

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 21, 2004, 20:24:10 ; Search time 303 Seconds
(without alignments)
5742.244 Million cell updates/sec

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Scoring table: OLIGO

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1342398 seqs, 321133274 residues

Word size: 1

Total number of hits satisfying chosen parameters: 2578168

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: listing first 45 summaries

Command line parameters:

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Database : Published Applications AA:

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Score	Match Length	ID	Description
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1	771	86.1	771	14	US-10-097-340-284	Sequence 284, App
2	771	86.1	771	14	US-10-262-538-10	Sequence 10, Appl
3	771	86.1	771	14	US-10-067-632-54	Sequence 54, Appl
4	771	86.1	771	14	US-10-247-671-164	Sequence 164, Appl
5	655	73.2	771	14	US-10-320-769-3	Sequence 3, Appl
6	151	16.9	151	9	US-09-864-761-47112	Sequence 47112, A
7	100	11.2	100	12	US-09-773-876-5	Sequence 5, Appl
8	154	6.0	54	14	US-10-029-386-30748	Sequence 30748, A
9	53	5.9	57	9	US-09-864-761-44075	Sequence 44075, A
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13	17	1.9	779	9	US-09-731-179-2	Sequence 2, Appl
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16	15	1.7	514	12	US-10-357-820-28	Sequence 28, Appl
17	15	1.7	636	16	US-10-408-785A-2003	Sequence 2003, Ap
18	15	1.7	749	14	US-10-263-538-12	Sequence 12, Appl
19	15	1.7	749	14	US-10-285-351B-1	Sequence 1, Appl
20	15	1.7	751	13	US-10-114-893-214	Sequence 214, App
21	15	1.7	751	14	US-10-060-036-172	Sequence 172, App
22	15	1.7	751	14	US-10-205-823-359	Sequence 359, App
23	15	1.7	751	14	US-10-262-538-14	Sequence 14, Appl
24	14	1.6	777	10	US-09-946-374-310	Sequence 310, Appl
25	14	1.6	777	12	US-10-206-915-348	Sequence 348, App
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ALIGNMENTS

RESULT 1
US-10-097-340-284
; Sequence 284, Application US/10097340
; Publication No. US20030087250A1
; GENERAL INFORMATION:
; APPLICANT: JOHN MONAHAN
; APPLICANT: Manjula GANNAVARAPU
; APPLICANT: Sebastian HOERSCH
; APPLICANT: Shubhangi KAMATKAR
; APPLICANT: Steve G. KOVATS
; APPLICANT: Rachel E. MEYERS
; APPLICANT: Michael MORRISSEY
; APPLICANT: Peter OLANDT
; APPLICANT: Ami SEN
; APPLICANT: Peter VEIBY
; APPLICANT: Gordon B. MILLIS
; APPLICANT: Robert C. BAST, Jr.
; APPLICANT: Karen LU
; APPLICANT: Rosemarie SCHMANDT
; APPLICANT: Xumei ZHAO
; APPLICANT: Karen GLATT
; TITLE OF INVENTION: Nucleic Acid Molecules and Proteins For The Identification,
; TITLE OF INVENTION: Assessment, Prevention, and Therapy of Ovarian Cancer
; FILE REFERENCE: MRI-030

; CURRENT APPLICATION NUMBER: US/10/097,340
 ; CURRENT FILING DATE: 2002-03-14
 ; PRIOR APPLICATION NUMBER: 60/276,025
 ; PRIOR FILING DATE: 2001-03-14
 ; PRIOR APPLICATION NUMBER: 60/325,149
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: 60/276,026
 ; PRIOR FILING DATE: 2001-03-14
 ; PRIOR APPLICATION NUMBER: 60/324,967
 ; PRIOR FILING DATE: 2001/09/26
 ; PRIOR APPLICATION NUMBER: 60/311,732
 ; PRIOR FILING DATE: 2001-08-10
 ; PRIOR APPLICATION NUMBER: 60/325,102
 ; PRIOR FILING DATE: 2001-09-26
 ; PRIOR APPLICATION NUMBER: 60/323,580
 ; PRIOR FILING DATE: 2001-09-19
 ; NUMBER OF SEQ ID NOS: 363
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 284
 ; LENGTH: 771
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 ; ORGANISM: Homo sapiens
 ; US-10-097-340-284

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; Publication No. US2003011324A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: NEUROPILIN/VEGF-C/VEGFR-3 MATERIALS AND METHODS
; FILE REFERENCE: 28967/37564
; CURRENT APPLICATION NUMBER: US/10/262,538
; CURRENT FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 771
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-538-10

Alignment Scores:
Pred. No.: 0 Length: 771
Score: 771.00 Matches: 771
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 86.15% Indels: 0
DB: 14 Gaps: 0

US-09-774-490-1 (1-2709) x US-10-262-538-10 (1-771)
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 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgArgGlnAspIleArgAsn 560
 1880 GGAGACCCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1939
 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro 580
 1940 GAAGAGAGATCATCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1999
 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
 2000 TCGCAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2059
 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgGlnGluArgLysGluGlu 620
 2060 ATCAGAGTGGATGATCATATCATCAGACAGATCAAGCGCTTCTGCTAGCTAGCTACAA 2119
 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuLeuLeuGln 640
 2120 CAGAGGATTCAGCAATTACTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2179
 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
 2180 CTTAAGGTAAACCTGGAAGTCAATTCACACAGAGATTTGGAAGAACTTCTTCATAAAGAT 2239
 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
 2240 GATGATGAGATGGCTTCAAGCAAGAAATGCTCAATGACATGCTGCTGCTGCTGCTGCTGCT 2299
 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
 2300 GTCTGCTACAGAGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2359
 701 ValTrpTyrArgAspPheMetGlnLeuLeuLeuHisHisProAsnLeuAsnThrMetAspGlu 720
 2360 TTCTGCTAACAGTTTGGAAAGGACCGCAAAACCAACCTCGGCAAGGCCGAGGACATACC 2419
 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740

2420 CCAGGACAGTACAAATCGAACCTTACAAAGATTAAGAAAGTGAAGACAGGAGG 2479
 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
 2480 ACCACCAATTTGAGAGCGCACCCAGGAGTGTC 2512
 761 ThrHisGluPheGluArgAlaProArgSerVal 771
 RESULT 3
 US-10-067-632-54
 ; Sequence 54, Application US/10067632
 ; Publication No. US20030166849A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Goodman, Corey S.
 ; Kolodkin, Alex L.
 ; Matthes, David
 ; Bentley, David R.
 ; O'Connor, Timothy
 ; TITLE OF INVENTION: The Semaphorin Gene Family
 ; NUMBER OF SEQUENCES: 100
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 Bush Street, Suite 3200
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/10/067,632
 ; FILING DATE: 04-Feb-2002
 ; CLASSIFICATION: <Unknown>
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/060,610
 ; FILING DATE: <Unknown>
 ; APPLICATION NUMBER: 08/835,268
 ; FILING DATE: <Unknown>
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Osman, Richard A.
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: B94-002-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415)343-4341
 ; TELEFAX: (415) 343-4342
 ; TELEX: <Unknown>
 ; INFORMATION FOR SEQ ID NO: 54:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 771 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; SEQUENCE DESCRIPTION: SEQ ID NO: 54:
 ; US-10-067-632-54
 Alignment Scores:
 Pred. No.: 0 Length: 771
 Score: 771.00 Matches: 771
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 86.15% Indels: 0
 DB: 14 Gaps: 0
 US-09-774-490-1 (1-2709) x US-10-067-632-54 (1-771)
 QY 200 ATGGGCTGGTTAACTAGGATTCGTCTGCTTTCTGGGAGTATTACTTACAGCAAGACGA 259
 Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20

QY 260 AACTATCAGATGGGAGAACCAATGTCGCAAGCTGAATATTCCTACAAAGAAATGTTG 319
Db |||||
21 AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCAACAATGTCATCTTCAATGCTTGGCCACACAGCTCCAGTTATCATACCTTC 379
Db |||||
41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
QY 380 CTTTGGATGAGAACGGAGTAGGCTGATGTTGTGAGCAAGATCAGATATTTTCATTC 439
Db |||||
61 LeuLeuAspGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGGTTAAATCAAGGATTTCAAAAGATGTTGTGGCCAGTATCTTACACCAAGAAGA 499
Db |||||
81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
QY 500 GATGAATCAAGTGGGCTGGAAAGACATCTCGAAGAAATGTCCTAAATTCATCAAGGTA 559
Db |||||
101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATAATCAGACTCACTGTGACGCTGTGGAACGGGGCTTTTCATCCAATT 619
Db |||||
121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTACATTCAAATTCAGACATCATCTGAGGACAATATTTTAAAGCTGGAGAACTCA 679
Db |||||
141 CysThrTyrIleGlnIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTGAAACGGCGTGGAGAGTCCATATGACCTTAAGCTGTCACAGCATCCCTT 739
Db |||||
161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGGAGAATTATPACTCTGGAAGTGGAGTGGATTTTATGGGGCGAGCTTTGCT 799
Db |||||
181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCGAACTCTTGGGACACACACCAATCAGGACAGACAGCATGATTCAGGTGG 859
Db |||||
201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCATATGATCCAAAGTTTCATAGTCCACCTCATCTCAGAGAGTGACAATCTCGAAGAT 919
Db |||||
221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATATCTTTCTCCGTGAAATGCAATAGATGGAGAACACTCTCGAAAGCT 979
Db |||||
241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ACTCAGCTAGATAGGTAGATATGCAAGATGCTTTGGAGGACAGAGAGTCTGGTG 1039
Db |||||
261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyHisArgSerLeuVal 280
QY 1040 AATAAATGACAAACATTCCTCAAGCTCGTCTGATTTGCTCAGTCCAGGTCCAATGGC 1099
Db |||||
281 AsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
QY 1100 ATTGACACTCATTTTGAACAATCGAGATGATTCCTTAAGAACTTTAAGATCCTAAA 1159
Db |||||
301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
QY 1160 AATCCAGTTGTATATGGAGTGTTCAGCTTCCAGTAAACATTTTCAAGGGATCAGCCGTG 1219
Db |||||
321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
QY 1220 TGTATGTATAGATGATGTGAGAGGGTGTTCCTTGGTCCATATGCCACAGGAT 1279
Db |||||
341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360
QY 1280 GGACCCAACTATCAATGGTGTCTTATCAAGAGAGTCCCTATCCACGGCCGAGACT 1339
Db |||||
361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
QY 1340 TGTCCCGACAAACATTTGGTGGTTTGTACTCTCAAAAGGACCTTCCTGATGATGTATATA 1399

Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspValIle 400
QY 1400 ACCTTTTCAAGAAAGTATCCAGCCATGACAAATCCAGTGTTCCTATGAACAATCGCCCA 1459
Db |||||
401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
QY 1460 ATAGTGATCAAAACGGATGTAATATTCAATTTACACAAATGTCGTAGACCGAGTGGAT 1519
Db |||||
421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
QY 1520 GCAGAAATGCAGACATGATGATGTTATGTTATCGGAACACAGATGTTGGACCGTCTTAAAA 1579
Db |||||
441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
QY 1580 GTAGTTTCAATTCCTAAGGAGACTGTTGATGATTTAGAGAGGTTCTGCTGGAAGAAATG 1639
Db |||||
461 ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluMet 480
QY 1640 ACAGTTTTCGGAAACCGACTGCTATTTCAGCAATGAGCTTTCCACTAAGCAGCAACAA 1699
Db |||||
481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGlnGln 500
QY 1700 CTATATATTGGTTCAACGGTGGGTTGCCAGCTCCCTTTTACACCGGTGTGATTTTAC 1759
Db |||||
501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
QY 1760 GGGAAACGGTGTCTGAGTGTCTCCCGCCGAGACCTTACTGTGCTTGGGATGGTTCT 1819
Db |||||
521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
QY 1820 GCATGTTCTCGCTATTTTCCACTGCAAGAGACGACAGACAGCAAGATATAAGAAAT 1879
Db |||||
541 AlaCysSerArgTyrPheProThrAlaLysArgThrArgGlnArgGlnAspIleArgAsn 560
QY 1880 GGAGACCCACTGACTCTGTTTCCAGACTTACACCATGATTAATCACAATGSCCAGCCCT 1939
Db |||||
561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisHisGlyHisSerPro 580
QY 1940 GAAGAGAAATCATCTATGCTGTAGAGATAGTAGCACATTTTGGAAATGCAGTCCGAAG 1999
Db |||||
581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
QY 2000 TCGCAGAGACGGTGTCTATTGGCAATTCAGAGCGGCAATGAAGAGCGAAAGAGAG 2059
Db |||||
601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluArgLysGluGln 620
QY 2060 ATCAGAGTGCATGATCATATCATCAGACAGATCAGAGCTTCTGCTAGTACTCTACAA 2119
Db |||||
621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
QY 2120 CAGAAGGATTCAGCGCAATTCCTCTGCCATGCGGTGGAACATGGTTTCATACAACTCTT 2179
Db |||||
641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
QY 2180 CTTAAGGTATACCTCGGAGCTTATGACAGACATTTGGAAGAACTTCTTCTATAAGAT 2239
Db |||||
661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluLeuLeuHisLysAsp 680
QY 2240 GATGATCGAGATCGCTCTTAAGACAAAGAAATGCTCAATAGCATGACACCTAGCCAGAAG 2299
Db |||||
681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
QY 2300 GTCTGTTACAGAGACTTCATGACGTTCATCAACCCCAATCTCAACAGATGGATGAG 2359
Db |||||
701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
QY 2360 TTCTGTGAACAAGTGTGGAAAGGGACCGAAACACACGCTCGGCAAAAGGGCCAGCACATACC 2419
Db |||||
721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
QY 2420 CCAGGGACAGTAACAAATGGAAGCACTTACAGAAATAAGAAAGTGAACAGGAG 2479

Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysGlyArgAsnArgArg 760

QY 2480 ACCCACGAATTTGAGAGGGCACCCAGAGTGTC 2512

Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 4

US-10-247-671-164

; Sequence 164, Application US/10247671

; Publication No. US20030194721A1

; GENERAL INFORMATION:

; APPLICANT: Mikita, Thomas

; APPLICANT: Shiffman, Dov

; APPLICANT: Porter, Gordon, J.

; APPLICANT: Kaser, Matthew R.

; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS

; FILE REFERENCE: PA-0050 US

; CURRENT APPLICATION NUMBER: US/10/247,671

; CURRENT FILING DATE: 2002-09-18

; PRIOR APPLICATION NUMBER: 60/323,784

; PRIOR FILING DATE: 2001-09-19

; NUMBER OF SEQ ID NOS: 186

; SOFTWARE: PERL Program

; SEQ ID NO 164

; LENGTH: 771

; TYPE: PRT

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: misc feature

; OTHER INFORMATION: Incyte ID No. US20030194721A1 1930967CD1

US-10-247-671-164

Alignment Scores:

Pred. No.:	0	Length:	771
Score:	771.00	Matches:	771
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	86.15%	Indels:	0
DB:	14	Gaps:	0

US-09-774-490-1 (1-2709) x US-10-247-671-164 (1-771)

QY 200 ATGGCTGGTTAACTAGGATTCTGTCTTTCTCGGAGTATTACTTACAGCAAGACCA 259

Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20

QY 260 AACTATCAGAAATGGGAGAACAAATGTGCCAGGCTGAAATTTATCTCAAGAAATCTTG 319

Db 21 AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40

QY 320 GAATCCAACAATGTATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCATACCTTC 379

Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60

QY 380 CTTTGGATCAGAACCGGAGTAGCTGTATGTGGAGCAAGATCAATTTTCATTC 439

Db 61 LeuLeuAspGluLysArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80

QY 440 GACCTGGTTAAATCAAGGATTTTCAAAAGATTGTGGCCAGTATCTTACACCAGAGA 499

Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100

QY 500 GATGAATGAATGGCTGGGAGAAACATCTCTGAAGATGTGCTAAATTTTCATCAAGGTA 559

Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120

QY 560 CTTAAGGCATATAATCAGACTCACCTGTACCGCTGTGGACGGGGCTTTTCATCCAAAT 619

Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140

QY 620 TGCACCTACATTTGAATTTGGACATCATCTCTGAGGACAAATATTTTAAAGCTGGAGACTCA 679

Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160

QY 680 CATTTTGAAAACGGCCGTGGGAGAGTCCATATGACCTTAAGCTGCTGACAGCATCCCTT 739

Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180

QY 740 TTAATAGATGGAGAATTATCTCTGGAATCAGCTGATTTTATGGGGCAGACTTTGCT 799

Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200

QY 800 ATCTTCCGAACTCTTTGGGACACCACCAATCAGGACAGACAGCAGCTATTTCCAGGTGG 859

Db 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTyr 220

QY 860 CTCATATGATCCAAAGTTTCAATAGTGGCCACCTCATCTCAGAGATGACATCTCTGAAGAT 919

Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240

QY 920 GACAAAGTATATCTTTCTTCGTTGAAATCAATAGATGGAGAACACTCTGGAAAAGCT 979

Db 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260

QY 980 ACTCAGCTAGATAGTTCAGATATGAAATGACCTTTGGAGGACACAGAGTCTGGTG 1039

Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280

QY 1040 AATAAATGACAAACATTTCTCAAGCTCGTCTGATTTGCTCAGTCCAGGTCCAAATGGC 1099

Db 281 AsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300

QY 1100 ATTGACACTCATTTTGTATGAACTCGAGATGTATCTTAATGAACCTTTAAAGATCCTAAA 1159

Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320

QY 1160 AATCCAGTTGTATATGGAGTCTTTACGACTTCCAGTAAACATTTTCAAGGATCAGCCGTG 1219

Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340

QY 1220 TGTATGTATAGATGAGTGTGAGAGGGTGTCTTGGTCCATATGCCCCACAGGAT 1279

Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360

QY 1280 GGACCCCACTCAATGGCTTATCAAGGAGAGTCCCTTATCACGCCGAGCAACT 1339

Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380

QY 1340 TGTCCCAACAAACATTTGGTGGTTTGAATCTACAAAGGACCTTCTGATGATGTATA 1399

Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400

QY 1400 ACCTTTGCAAGAAGTTCATCCAGCCATGTACAATCCAGTGTTCCTATGAACATTCGCCCA 1459

Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420

QY 1460 ATAGTGAATCAAAACGGATGTAATTAATCAATTTACAAATTCGATAGACCGAGTGGAT 1519

Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440

QY 1520 GCAGAAGATGACAGATGATGTATGTTTATCGGAACAGATCTTGGGACCGTCTCTTAAA 1579

Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460

QY 1580 GTAGTTTCAATTCCTAAGGACACTTGTGTATGATTTAGAGAGGTCTCTCTGGAAGAAATG 1639

Db 461 ValValSerIleProLysGluThrTyrTyrAspLeuGluValLeuLeuGluMet 480

QY 1640 ACAGTTTTCGGGAACCGACTGTCTTATTCAGCAATGAGCTTTCCACTTAAGCAGCAACAA 1699

Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500

QY 1700 CTATATATTTGGTCAACGGCTGGGGTGGCCAGCTCCCTTTACACCGGTGTGATTTTAC 1759

Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520

QY 1760 GGAAGCGTGTGCTGAGTGTTCCTCGCCCGAGACCTTACTGTGCTGTGGATGTTCT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
QY 1820 GCATGTTCTCGCTATTTTCCCACTGCAAGACACCAAGACGACCAAGATATAAGAAAT 1879
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgThrArgArgGlnAspIleArgAsn 560
QY 1880 GGAGACCCACTGACTCATCTGTTTCAGACTTACACCATGATTAATCACCATGGCCACAGCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro 580
QY 1940 GAAGAGAGAAATCATCTATGCTGTAGAGATAGTACACATTTTTCGAATGTCAGTCCGAAG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
QY 2000 TCCGAGAGAGCCCTCGTCTATTGGCAATTCAGAGCGGCAATGAAGAGCGAAAGAGAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluArgLysGluGln 620
QY 2060 ATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCCTTCTGCTAGTACTACAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
QY 2120 CAGAAGGATTTCAGGCAATTACCTCTGCCATGCGGTGGAACATGGGTTTCATACAACTCTT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
QY 2180 CTTAAGGTAAACCTCGAAGTCAATTGACACAGAGCATTTGGAGAACTTCTTCATAAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
QY 2240 GATGATGAGATGGCTCTAAGACCAAGAAATGTCCATAGCATGACACCTAGCCAGAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
QY 2300 GTCTCGTACAGAGACTTCATGACGCTCATCAACCAACCCCAATCTCAACACCATGGATGAG 2359
Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
QY 2360 TTCTCTGACACAGTTTGAAGAGGACCGAAACACACCTCGGCAAGCCAGGACATACC 2419
Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
QY 2420 CCAGGGAACAGTAAACAAATGGAAGCACTTACAAGAAAATAAGAAAGGTAGAAACAGGAGG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
QY 2480 ACCACGATTTGAGAGGCGCCACCCAGAGGTGC 2512
Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 5

US-10-320-769-3
; Sequence 3, Application US/10320769
; Publication No. US20030158402A1
; GENERAL INFORMATION:
; APPLICANT: HALL, Kathryn T.
; APPLICANT: FREEMAN, Gordon J.
; APPLICANT: SCHULTZE, Joachim L.
; APPLICANT: BOUSSOTIS, Vassiliki
; APPLICANT: NADLER, Lee M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DFN-005CPA2,
; CURRENT APPLICATION NUMBER: US/10/320,769
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: US/08/556,422
; PRIOR FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 655
; TYPE: PRT

; ORGANISM: Homo sapiens
US-10-320-769-3

Alignment Scores:
Pred. No.: 0 Length: 655
Score: 655.00 Matches: 655
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 73.18% Indels: 0
DB: 14 Gaps: 0

US-09-774-490-1 (1-2709) x US-10-320-769-3 (1-655)

QY 200 ATGGGCTGTTAACTAGGATTGTCTGCTTTCTGGGAGTATTACTTACAGCAAGAGCA 259
Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
QY 260 AACTATCAGAAATGGGAAGAACAAATGTGCCAAGCTGAAATTTATCTTACAAAGAAATGTTG 319
Db 21 AsnTyrGlnAsnGlnLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCAAATGTGATCACTTTCAATGGCTTGGCCAAAGCTCCAGTTATCATCACTTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerSerTyrHisThrPhe 60
QY 380 CTTTTCGATGAGCAAGCGAGTAGCTGTATGTTGGAGCAAGAGGATCACATATTTTCATTC 439
Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGTTTAATATCAAGGATTTTCAAAAGATTGTGTGGCCAGTATCTTACACCAAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpValSerTyrThrArgArg 100
QY 500 GATGAATGCAAGTGGCTGGAAAAGACATCTGAAAAGATGCTCAATTTTCATCAAGGTA 559
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATTAATCAGACTCACTTGTACGCTGTGGAACGGGGGCTTTTCATCCAAAT 619
Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTACATTTGAAATTTGGACATCATCTCTGAGGACAAATATTTTAAAGCTGGAGACTCA 679
Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTGAACCGCGCTGGAGAGTCCATATGACCTTAAGCTGTGACAGCATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGGAGATTTATATCTTGGAACTGCAGCTGATTTTATGGGGCGAGACTTTGCT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCGAACTCTTGGCACCAACCACTTACAGACAGAGAGAGATCATCTCCAGTGG 859
Db 201 IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCATATGATCCAAAGTTTCAATAGTGGCCACCTCATCTCAGAGAGTGACAAATCTCAAGAT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATCTTTTCTTCGTTGAAAATGCAATAGATGGAGAACACTCTGGAAAAGCT 979
Db 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ACTCAGCTAGATAGTGTGAGATATGCAAGATGACTTTGGAGGGGACAGAGACTCTGGG 1039
Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
QY 1040 AATAAATGACACATCTCTCAAAAGTCTCTGATTTGCTGATTTGCTGACAGGTCAATGCG 1099
Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300

QY 1100 ATTGACACTCATTTTGGATGAGTGCAGGATGATTCCTTAATGAACTTTAAAGATCCCTAAA 1159
 Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProlys 320
 QY 1160 AATCCAGTGTATATGAGTGTGTACGACTTCAGTAACATTTTCAAGGGATCAGCGGTG 1219
 Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
 QY 1220 TGATGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1279
 Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360
 QY 1280 GGACCAACTATCAATGGGTGCTTATCAAGGAAGTCCCTATCCACGCGCCAGGAAT 1339
 Db 361 GlyProAsnTyrGlnTyrValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
 QY 1340 TGTCGACGCAAAACATTTGGTGTGTGTGCTCTCAAGAGACCTTCCTGATGATGATGAT 1399
 Db 381 CysProSerTyrThrPheGlyGlyPheAspSerThrLysAspLeuProAspValVal 400
 QY 1400 ACCTTTGCAAGAGTCTATCCAGCCATGATCAATCCAGTGTTCCTATCAACAATCGCCCA 1459
 Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
 QY 1460 ATAGTATCAAAACGAGTAAATATCAATTTACAAATTCGATGATGATGATGATGATGATGAT 1519
 Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspValAsp 440
 QY 1520 GCAGAAGATGGACAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1579
 Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
 QY 1580 GTAGTTTCAATTCCTAAGAGACTTGGTATGATGATGATGATGATGATGATGATGATGATGAT 1639
 Db 461 ValValSerIleProLysGlnTyrTrpTyrAspLeuGluGluValLeuGluGluMet 480
 QY 1640 ACAGTTTTCGGGAACCGACTCTATTCAGCAATGGAGCTTCCACTAAGCAGCAACAA 1699
 Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
 QY 1700 CTATATATTGGTTCAAGCTGGGTGCTCCAGTCTCTTACACCGGTGATGATGATGATGAT 1759
 Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
 QY 1760 GCGAAGCGTGTGCTGAGTGTGCTCGCCGAGACCTTACTGTGCTGGATGATGATGATGAT 1819
 Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaIleTrpAspGlySer 540
 QY 1820 GATGTTCTGCTATTTTCCACTCCAAAGAGAGCAGCAAGCAGCAAGATATAAGAAAT 1879
 Db 541 AlaCysSerArgTyrPheProThrAlaLysArgThrArgArgGlnAspIleArgAsn 560
 QY 1880 GGAGACCCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1939
 Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro 580
 QY 1940 GAAGAGAGATCATCTATGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1999
 Db 581 GluGluArgIleIleTyrGlyValGluAsnSerThrPheLeuGluCysSerProLys 600
 QY 2000 TCGCAGAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2059
 Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgGlnGluArgGlyGluGlu 620
 QY 2060 ATCAGAGTGGATGATCATATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 2119
 Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
 QY 2120 CAGAGAGATTTCAGCAATTTACCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2164
 Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGly 655

US-09-864-761-47112
 ; Sequence 47112, Application US/09864761
 ; Patent No. US20020048761A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; FILE REFERENCE: Aemica-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; PRIORITY FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/235,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 09/608,408
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 09/774,203
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 49117
 ; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 47112
 ; LENGTH: 151
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: MAP TO AC006322.2
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.73
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.55
 ; OTHER INFORMATION: SWISSPROT HIT: Q14563, EVALUE 2.00e-88
 US-09-864-761-47112
 Alignment Scores:
 Pred. No.: 5.29e-138 Length: 151
 Score: 151.00 Matches: 151
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 16.87% Indels: 0
 DB: 9 Gaps: 0
 US-09-774-490-1 (1-2709) x US-09-864-761-47112 (1-151)
 QY 2060 ATCAGAGTGGATGATCATATCATCATCATCATCATCATCATCATCATCATCATCATCATCAT 2119

US-09-774-490-1 (1-2709) x US-09-773-876-5 (1-100)

QY	1211	TCAGCCGTGTGATGTATAGCATGAGTGATGAGAAGGTGTTCCTTGGTCCATATGCC	1270
Db	1	SerAlaValCysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAla	20
QY	1271	CACAGGANTGGACCCAACTATCAATGGTGCCTTATCAAGAAAGAGTCCCTCATCCACGG	1330
Db	21	HisArgAspGlyProAsnTyrGlnTyrValProTyrGlnGlyArgValProTyrProArg	40
QY	1331	CCAGGAACCTGTCCACGAAACATTTCGTGGTTTTCACCTACAAAGGACCTTCCTGAT	1390
Db	41	ProGlyThrCysProSerLysThrPheGlyPheAspSerThrLysAspLeuProAsp	60

US-09-774-490-1 (1-2709) x US-10-029-386-30748 (1-54)

Qy	1691	CAGCAACAAC	TATATTTGGTT	CAACGGCTGGGGTT	GCCAGAGTCCCTTTACACCGGTG	1750
Db	1	GinGlnGln	LeuTyrlleGly	SerThrAlaGly	ValAlaGlnLeuProLeuHisArgCys	20
Qy	1751	GATATTTACGGG	AAACGCTGTGCT	GAGTGTGCTCGCCG	CAGACCCCTTACTGTGCTTGG	1810
Db	21	AspIleTyrGly	AlaCysAlaGlu	CysLeuAlaArgAsp	ProTyrCysAlaTrp	40
Qy	1811	GATGGTCTGC	ATGTTCTCGCTAT	TTTCCCACTGC	AAAGAGA	1852
Db	41	AspGlySerAla	CysSerArgTyr	PheProThrAla	AlaLysArg	54

```

RESULT 9
US-09-864-761-44075
; Sequence 44075, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCES: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864, 761
; CURRENT FILING DATE: 2001-05-23
USE

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; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; PRIOR APPLICATION NUMBER: PCT/US01/00666
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00667
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00664
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00669
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00665
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00668
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00663
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00662
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00661
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: PCT/US01/00670
 ; PRIOR FILING DATE: 2001-01-30
 ; PRIOR APPLICATION NUMBER: US 60/234,687
 ; PRIOR FILING DATE: 2000-09-21
 ; PRIOR APPLICATION NUMBER: US 09/608,408
 ; PRIOR FILING DATE: 2000-06-30
 ; PRIOR APPLICATION NUMBER: US 09/774,203
 ; PRIOR FILING DATE: 2001-01-29
 ; NUMBER OF SEQ ID NOS: 49117
 ; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 44075
 ; LENGTH: 57
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: MAP TO AC004848.1
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
 ; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
 ; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
 ; OTHER INFORMATION: SWISSPROT HIT: Q14563, EVALUATION 5.00e-25
 ; US-09-864-761-44075

Alignment Scores:
 Pred. No.: 3.9e-42 Length: 57
 Score: 53.00 Matches: 53
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.92% Indels: 0
 DB: 9 Gaps: 0

US-09-774-490-1 (1-2709) x US-09-864-761-44075 (1-57)
 QY 311 GAAATGTTGGAATCCAAATGTGATCATTTCATGCTGGCCAAAGTCAGTTAT 370
 Db 5 GluMetLeuGluSerAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyr 24
 QY 371 CATACCTTCCTTTGGATGAGGAGGAGTAGGCTGTATGTTGGAGCAAGATCACATA 430
 Db 25 HisThrPheLeuLeuAspGluArgSerArgLeuTyrValGlyAlaLysAspHisIle 44
 QY 431 TTTTCATTTCGACCTGTTAATATCAAGGATTTTCAAAAG 469

Db 45 PheSerPheAspLeuValAsnIleLysAspPheGlnLys 57

RESULT 10
 US-10-029-386-29372
 ; Sequence 29372, Application US/10029386
 ; Publication No. US20030194704A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
 ; FILE REFERENCE: AEONICA-X-2
 ; CURRENT APPLICATION NUMBER: US/10/029,386
 ; CURRENT FILING DATE: 2001-12-20
 ; NUMBER OF SEQ ID NOS: 34288
 ; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
 ; SEQ ID NO 29372
 ; LENGTH: 60
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: MAP TO CHR7.1
 ; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.5
 ; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.68
 ; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.64
 ; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.7
 ; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.69
 ; OTHER INFORMATION: SWISSPROT HIT: Q14563, EVALUATION 5.00e-25
 ; US-10-029-386-29372

Alignment Scores:
 Pred. No.: 3.88e-42 Length: 60
 Score: 53.00 Matches: 53
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 5.92% Indels: 0
 DB: 14 Gaps: 0

US-09-774-490-1 (1-2709) x US-10-029-386-29372 (1-60)
 QY 311 GAAATGTTGGAATCCAAATGTGATCATTTCATGCTGGCCAAAGTCAGTTAT 370
 Db 4 GluMetLeuGluSerAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyr 23
 QY 371 CATACCTTCCTTTGGATGAGGAGGAGTAGGCTGTATGTTGGAGCAAGATCACATA 430
 Db 24 HisThrPheLeuLeuAspGluArgSerArgLeuTyrValGlyAlaLysAspHisIle 43
 QY 431 TTTTCATTTCGACCTGTTAATATCAAGGATTTTCAAAAG 469
 Db 44 PheSerPheAspLeuValAsnIleLysAspPheGlnLys 56

RESULT 11
 US-09-864-761-44552
 ; Sequence 44552, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharron G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
 ; FILE REFERENCE: Aeomica-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03

;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 44552
;; LENGTH: 41
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC006322.2
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.46
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.54
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.56
;; OTHER INFORMATION: EST HUMAN HIT: BF700780.1, EVALUATE 1.00e-17
;; OTHER INFORMATION: SWISSPROT HIT: Q14563, EVALUATE 1.00e-18
US-09-864-761-44552

Alignment Scores:
Pred. No.: 2,2e-30 Length: 41
Score: 41.00 Matches: 41
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 4.58% Indels: 0
DB: 9 Gaps: 0

US-09-774-490-1 (1-2709) x US-09-864-761-44552 (1-41)

QY 1937 CTTGAGAGAGATCATCTATGCTAGAGATAGACATTTTGGATGAGTCGC 1996
Db 1 ProGluGluArgIleIleTyrglyValGluAsnSerSerThrPheLeuGluCysSerPro 20
QY 1997 AAGTCGACAGAGCGCTGGTCTATTGGCAATTCAGAGCGGAAATGAAGAGCGGAAAGAA 2056
Db 21 LysSerGlnArgAlaLeuValTyTrpGlnPheGlnArgAsnGluGluArgGlySglu 40

QY 2057 GAG 2059
Db 41 Glu 41

RESULT 12

US-09-864-761-39708
; Sequence 39708, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.

;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; FILE REFERENCE: Aecomica-X-1
;; CURRENT APPLICATION NUMBER: US/09/864,761
;; CURRENT FILING DATE: 2001-05-23
;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 39708
;; LENGTH: 33
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC004848.1
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.7
;; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.5
;; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.6
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.5
;; OTHER INFORMATION: SWISSPROT HIT: Q14563, EVALUATE 4.00e-15
US-09-864-761-39708

Alignment Scores:
Pred. No.: 1.5e-22 Length: 33
Score: 33.00 Matches: 33
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3.69% Indels: 0
DB: 9 Gaps: 0

US-09-774-490-1 (1-2709) x US-09-864-761-39708 (1-33)

QY 533 AAAGAATGCTGCTAATTTTCATCAAGGACTTAAGGCATATATCAGACTACTTGTACGCC 552

Db 1 LysGluCysAlaAsnPhlelleLysvalleuLysAlaTyraSnGlnThrHisLeuTyAla 20

Qy 593 TGTGAACGGGGGTTTTCATCCAAATTTGCACCTACATT 631

Db 21 CysGlyThrGlyAlaPheHisProileCysThrTyxile 33

RESULT 13

US-09-731-179-2
; Sequence 2, Application US/09731179
; Patent No. US20010049432A1
; GENERAL INFORMATION:
; APPLICANT: Holloway, James L..
; APPLICANT: Foley, Kevin P..
; TITLE OF INVENTION: HUMAN SEMAPHORIN ZSMF-16
; FILE REFERENCE: 99-90
; CURRENT APPLICATION NUMBER: US/09/731,179
; PRIOR FILING DATE: 2000-12-06
; PRIOR APPLICATION NUMBER: US 60/169,238
; PRIOR FILING DATE: 1999-12-06
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 779
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-09-731-179-2

Alignment Scores:
Pred. No.: 4.42e-07 Length: 779
Score: 17.00 Matches: 17
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.90% Indels: 0
Gaps: 0

US-09-774-490-1 (1-2709) x US-09-731-179-2 (1-779)

Qy 1766 GCGTGTGCTGAGTGTGCTGCCCGAGACCTTACTGTGCTGGGATGGT 1816

Db 525 AlaCysAlaGluCysCysLeuAlaArgAspProTyCysAlaTrpAspGly 541

RESULT 14

US-09-813-290-4
; Sequence 4, Application US/09813290
; Patent No. US20020042504A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L..
; APPLICANT: Hilbun, Erin
; APPLICANT: Turner, C. Alexander Jr..
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; TITLE OF INVENTION: No. US20020042504A1 Human Secreted Proteins and Polynucleotides
; FILE REFERENCE: LEX-0151-USA
; CURRENT APPLICATION NUMBER: US/09/813,290
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,638
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 60/191,188
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 60/193,639
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 782
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-813-290-4

Alignment Scores:

Pred. No.: 4.42e-07 Length: 782
Score: 17.00 Matches: 17
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.90% Indels: 0
Gaps: 0

US-09-774-490-1 (1-2709) x US-09-813-290-4 (1-782)

Qy 1766 GCGTGTGCTGAGTGTGCTGCCCGAGACCTTACTGTGCTGGGATGGT 1816

Db 528 AlaCysAlaGluCysCysLeuAlaArgAspProTyCysAlaTrpAspGly 544

RESULT 15

US-09-813-290-2
; Sequence 2, Application US/09813290
; Patent No. US20020042504A1
; GENERAL INFORMATION:
; APPLICANT: Walke, D. Wade
; APPLICANT: Wilganowski, Nathaniel L..
; APPLICANT: Turner, C. Alexander Jr..
; APPLICANT: Hilbun, Erin
; APPLICANT: Wang, Xiaoming
; APPLICANT: Donoho, Gregory
; TITLE OF INVENTION: No. US20020042504A1 Human Secreted Proteins and Polynucleotides
; FILE REFERENCE: LEX-0151-USA
; CURRENT APPLICATION NUMBER: US/09/813,290
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: US 60/190,638
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: US 60/191,188
; PRIOR FILING DATE: 2000-03-22
; PRIOR APPLICATION NUMBER: US 60/193,639
; PRIOR FILING DATE: 2000-03-31
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 875
; TYPE: PRT
; ORGANISM: homo sapiens
US-09-813-290-2

Alignment Scores:

Pred. No.: 4.35e-07 Length: 875
Score: 17.00 Matches: 17
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.90% Indels: 0
Gaps: 0

US-09-774-490-1 (1-2709) x US-09-813-290-2 (1-875)

Qy 1766 GCGTGTGCTGAGTGTGCTGCCCGAGACCTTACTGTGCTGGGATGGT 1816

Db 621 AlaCysAlaGluCysCysLeuAlaArgAspProTyCysAlaTrpAspGly 637

Search completed: September 21, 2004, 21:18:30

Job time : 343 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 21, 2004, 19:47:54 ; Search time 53.5 Seconds
(without alignments)

5228.215 Million cell updates/sec

Title:

Perfect score: 895

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Ygapop 60.0 , Ygapext 60.0
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 389414 seqs, 51625971 residues

Word size: 1

Total number of hits satisfying chosen parameters: 663654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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-OUTFMT=ptc -NORM=ext -HEAPSIZES=500 -MINLEN=0 -MAXLEN=2000000000
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Database :

Issued Patents AA:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	771	86.1	771	1	US-08-121-713D-54
2	771	86.1	771	1	US-08-835-268-54
3	771	86.1	771	2	US-09-060-692-54
4	771	86.1	771	3	US-08-833-391-54
5	771	86.1	771	4	US-09-060-610-54
6	771	86.1	771	5	PCT-US94-10151A-54
7	655	73.2	655	4	US-08-556-422A-3
8	434	48.5	477	1	US-08-136-922-2
9	13	1.5	775	4	US-09-308-179B-1
10	10	1.1	606	3	US-09-041-236-4
11	10	1.1	606	4	US-09-771-467C-4
12	9	1.0	112	4	US-09-341-461-34

13	9	1.0	295	4	US-08-556-422A-6	Sequence 6, Appli
14	9	1.0	425	4	US-08-556-422A-7	Sequence 7, Appli
15	9	1.0	607	4	US-08-556-422A-4	Sequence 4, Appli
16	9	1.0	690	4	US-09-252-991A-32350	Sequence 22350, A
17	9	1.0	862	4	US-08-556-422A-2	Sequence 2, Appli
18	9	1.0	913	4	US-08-971-089-4	Sequence 4, Appli
19	8	0.9	57	4	US-09-152-060-58	Sequence 58, Appli
20	8	0.9	139	4	US-09-252-991A-24681	Sequence 24681, A
21	8	0.9	332	4	US-09-252-991A-32158	Sequence 32158, A
22	8	0.9	360	4	US-09-252-991A-20193	Sequence 20193, A
23	8	0.9	374	1	US-08-464-148-2	Sequence 2, Appli
24	8	0.9	374	1	US-08-385-500-2	Sequence 2, Appli
25	8	0.9	374	1	US-08-846-784-2	Sequence 2, Appli
26	8	0.9	454	3	US-09-080-044-4	Sequence 4, Appli
27	8	0.9	454	4	US-09-531-857A-4	Sequence 4, Appli
28	8	0.9	673	4	US-09-252-991A-25962	Sequence 25962, A
29	8	0.9	849	4	US-09-157-257-4	Sequence 4, Appli
30	7	0.8	17	1	US-08-644-456-1	Sequence 1, Appli
31	7	0.8	28	1	US-08-164-151-22	Sequence 22, Appli
32	7	0.8	37	4	US-09-574-377-27	Sequence 27, Appli
33	7	0.8	43	4	US-09-205-258-296	Sequence 296, App
34	7	0.8	46	4	US-09-369-247-82	Sequence 82, Appli
35	7	0.8	48	4	US-09-489-847-175	Sequence 175, App
36	7	0.8	49	4	US-09-716-129-71	Sequence 71, Appli
37	7	0.8	62	4	US-08-328-352-7261	Sequence 7261, Ap
38	7	0.8	62	4	US-09-621-976-6807	Sequence 6807, Ap
39	7	0.8	62	6	5320958-24	Patent No. 5320958
40	7	0.8	67	4	US-09-107-532A-4497	Sequence 4497, Ap
41	7	0.8	68	2	US-08-456-647B-31	Sequence 31, Appli
42	7	0.8	68	2	US-08-237-401A-31	Sequence 31, Appli
43	7	0.8	69	4	US-09-134-001C-5401	Sequence 5401, Ap
44	7	0.8	70	4	US-08-621-976-5508	Sequence 5508, Ap
45	7	0.8	70	4	US-09-621-976-5563	Sequence 5563, Ap

ALIGNMENTS

RESULT 1
US-08-121-713D-54
; Sequence 54, Application US/08121713D
; Patent No. 5639856
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713D
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELEX:

INFORMATION FOR SEQ ID NO: 54:

SEQUENCE CHARACTERISTICS:
 LENGTH: 771 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-121-713D-54

Alignment Scores:

Pred. No.: 0 Length: 771
 Score: 771.00 Matches: 771
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 86.15% Indels: 0
 Gaps: 0

US-09-774-490-1 (1-2709) x US-08-121-713D-54 (1-771)

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Db	1	MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla	20
QY	260	AACTATCAGATGGGAAGCAAAATGTCAGAGGCTGAAATTTATCTCAAAAGAAATGTTG	319
Db	21	AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu	40
QY	320	GAATCCAAATGATCACTTTCAATGGCTGGCCCAACAGCTCCAGCTTATCATCTTC	379
Db	41	GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerSerTyrHisThrPhe	60
QY	380	CTTTTGGATGAGACCGAGTAGCTGTATGTCGAGCAAGAGATCATATTTTCATTC	439
Db	61	LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe	80
QY	440	CACCTGGTTAATATCAAGGATTTTCAAAAGATTGTGGCCAGTATCTTACACAGAGA	499
Db	81	AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg	100
QY	500	GATGATCAAGTGGCGTGGAAAAGACATCTGTAAGAAATGTGCTAATTTTCATCAGGTA	559
Db	101	AspGluCysLysTrpAlaGlyLysAspLeuLysGluCysAlaAsnPheIleLysVal	120
QY	560	CTTAAGGCATATAATCAGACTCACTTGACGCTGTGGAAAGGGGGCTTTTCATCCAATT	619
Db	121	LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle	140
QY	620	TGCACCTACATGAATTTGGACATCATCTGAGGACAAATATTTTAAGCTGGAGAACTCA	679
Db	141	CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer	160
QY	680	CATTTTGAACCGCGGGAAGAGTCCATATGACCTAAGCTGCTGACAGCATCCCTT	739
Db	161	HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu	180
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Db	181	LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla	200
QY	800	ATCTTCCGAATCTTGGCACCCACCATCAGGACAGCAGCATGATTCAGAGTGG	859
Db	201	IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp	220
QY	860	CTCAATGATCAAAAGTTCATTAGTGGCCACCTCATCTCAGAGAGTGACATCTCGAAGAT	919
Db	221	LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp	240
QY	920	GACAAAGTACTTTTCTCCGTGAAAATGCAATAGATGAGACACTCTCGGAAAAGCT	979
Db	241	AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla	260
QY	980	ACTCAGCTAGAAATAGTACATATGCAAGAAATGACATTTGGAGGCGCAGAAAGTCTGCTG	1039
Db	261	ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal	280

QY	1040	AATAAATCGAACAAATCTCTCAAGCTGCTGTGATTTGCTCAGTGCAGGTCGAAATGGC	1099
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QY	1100	ATTGACACTCATTTTGATGAACTGCAGGATGATTTCTTAATGAACCTTTAAAGATCTTAAA	1159
Db	301	IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys	320
QY	1160	AATCCAGTTGTATATGGAGTGTTTACGACTTCCAGTAAACATTTTCAAGGGATCAGCGGT	1219
Db	321	AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal	340
QY	1220	TGTATGTATAGATGAGTGTGAGAGGGTGTCTTGGTCCATATGCCACAGGAT	1279
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QY	1280	GGACCAACTATCAATGGTGGCTTTATCAAGAGAGTCCCTTATCCACGGCCAGGAAC	1339
Db	361	GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr	380
QY	1340	TGTCCAGCAAAACATTTGGTGGTTTGCATCTACAAAGGACCTTCTGTATGATGTATA	1399
Db	381	CysProSerLysThrPheGlyPheAspSerThrLysAspLeuProAspAspValIle	400
QY	1400	ACCTTTGCAAGAAGTCATCCAGCCATGACAAATCCAGTGTTCCTATGAACAATCGCCCA	1459
Db	401	ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro	420
QY	1460	ATAGTGATCAAAACCGATGTAAATTTACAAATTTACAAATTTGCTAGACCGAGTGGAT	1519
Db	421	IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp	440
QY	1520	GCAGAGATGACAGTATGATGTATGTTATCGGAACAGATGTTGGACCGTCTTAAA	1579
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QY	1580	GTAGTTTCAATTCCTAAGGAGACTTGGTATGATTAGAGAGGTTCTGCTCGAAGAAATG	1639
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QY	1700	CTATATATTGGTTCAACGGCTGGGGTTCGCCAGTCCCTTTACACCGGTGTGATATTAC	1759
Db	501	LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr	520
QY	1760	GGGAAAGCGTGTGAGTGTGCTCGCCGAGACCTTACTTACTGTGCTGGATGGTTCT	1819
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QY	1820	GCATGTCTCTCGCTATTTTCCCACTGCAAGAGAGACCAAGACGACCAAGATATAAGAAAT	1879
Db	541	AlaCysSerArgTyrPheProThrAlaLysArgThrArgArgGlnAspIleArgAsn	560
QY	1880	GGAGACCCACTGACTCACTGTTTACAGACTTACACCATGATAATTCACATGGCCACGCT	1939
Db	561	GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisGlyHisSerPro	580
QY	1940	GAAGAGAGATCATCTATGCTGTAGAGATAGTACACATTTTTCGAATGTCAGTCCGAG	1999
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QY	2000	TCCGAGAGAGCGCTGCTTATTGGCAATTTCCAGAGCGCAATTAAGAGCGAAAGAAAG	2059
Db	601	SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu	620
QY	2060	ATCAGAGTGGATCATATCATCAGGACAGTCAAGCCCTTCTGCTACGTAGTCTACAA	2119
Db	621	IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln	640

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D 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
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D 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 2

US-08-835-268-54
; Sequence 54, Application US/08835268
; Patent No. 5807826
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,268
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-835-268-54

Alignment Scores:
Pred. No.: 0 Length: 771
Score: 771.00 Matches: 771
Percent Similarity: 100.00% Conservatives: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 86.15% Indels: 0
DB: 1 Gaps: 0

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QY 320 GAATCCAACAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATCCTTC 379
D 41 GluSerAsnValIleThrPheAsnGlyLeuAlaAsnSerSerSerTyrHisThrPhe 60
QY 380 CTTTGGATGAGGACGGAGTAGGTGTATGTTGGAGCAAGATACACATATTTTCATTC 439
D 61 LeuLeuAspGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGTTAATATCAAGGATTTTCAAAAGATTGTGTGCCAGTATCTTACACCAAGACA 499
D 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
QY 500 GATGAATGCAAGTGGCTCGAAAAGACATCTCGAAGATGCTGAATTTTCATCAAGTA 559
D 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATAATCAGACTCACTTGACGGCTGTGGAACGGGGCTTTTCATCAAT 619
D 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTACATTGCAATTCGACATCATCTGAGGACATATTTTAAAGCTGAGAACTCA 679
D 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTGAACGGCGTGGAGAGTCCATATGACCTTAAGCTGCTGACACATCCCTT 739
D 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGGAGAAATTATATCTGGAAGTGGAGCTGATTTTATGGGCGAGACTTTGCT 799
D 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCGAACTCTGGGACACCAACCAATCAGACAGACAGCATGATTCAGGTGG 859
D 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCAATGATCCAAAGTTCAATTAGTGCCACCTCATCTCAGAGAGTGACAAATCCTGAAGAT 919
D 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATATCTTTCTTCGCGTGAATGCAATAGATGAGAGACACTCTCGAAAGCT 979
D 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ACTCAGCTAGAAATAGGTGAGATATGCAAGATGACTTTGGAGGGGACAGAGTCTGGTG 1039
D 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyHisArgSerLeuVal 280
QY 1040 AATAAATGGACACATCTCTCAAGCTCGTCTGATTTGCTAGTGCCAGGTCAAAATGCC 1099
D 281 AsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
QY 1100 ATTGACACTCATTTTATGATGAACCTGCAGGAGTGTATTCCTTAATGACTTAAAGATCCTAAA 1159

Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPhelYsAspProLys 320
Qy 1160 AATCCAGTTGTATATGAGTGTTCAGACTTCAGTAACATTTCAAGGGATCAGCCG 1219
Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePhelYsGlySerAlaVal 340
Qy 1220 TGTATGTATAGCATCAGTGTGAGAAAGGTTCTCTGTCATATGCCACAGGAT 1279
Db 341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360
Qy 1280 GGACCCAACTATCAATGGGTCTTATCAAGAGAGTCCCTATCCACGCCCAGAACT 1339
Db 361 GlyProAsnTyrGlnTyrValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
Qy 1340 TGTCGCCAGCAAAACATTTGGTGGTTTGACTCTACAAAGACCTTCTGATGATGTATA 1399
Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400
Qy 1400 ACCTTTCAAGAGACTATCCAGCCCATCAATCCAGTGTTCCTATGAACAATCCGCCA 1459
Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
Qy 1460 ATAGTGATCAAAACGGATGAAATTAATCAATTTACAAATTCGTPAGACCGAGTGGAT 1519
Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
Qy 1520 CCAGAAGATGACAGTATGATGTTATGTTATCGGAACAGATGTGGACCGTCTTAA 1579
Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
Qy 1580 GTAGTTTCAATCTTAGGAGACTGTGTATGATTAATAGAGGTTCTGCTGGAGAAATG 1639
Db 461 ValValSerIleProLysGluThrTyrAspLeuGluValLeuLeuGluGluMet 480
Qy 1640 ACAGTTTTCGGGAACCGACTGCTATTTTCAGCAATGAGCTTTCACATAGACGACAA 1699
Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
Qy 1700 CTATATATGTTCAACGGCTGGGTTGCCAGCTCCCTTTACCCGGTGTATATTAC 1759
Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
Qy 1760 GGGAAAGCTGTGCTGAGTGTGCTCGCCGAGACCTTACTGTGCTGGATGGTCT 1819
Db 521 GlyLysAlaCysAlaGluCysSerLeuAlaArgAspProTyrCysAlaTyrAspGlySer 540
Qy 1820 GCATGTTCTCGCTATTTCCCACTGCCAAGACGCGCAAGACGCAAGATATAAGAAAT 1879
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgArgGlnAspIleArgAsn 560
Qy 1880 CGAGACCCACTGACTCATCTGTCAGACTTACACCATGATATCACCATGGCCACAGCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisGlyHisSerPro 580
Qy 1940 GAAGAGAAATCATCTATGTTGTAGAAATAGTACACATTTTGGATCGAGTCCGAAG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerThrPheLeuGluCysSerProLys 600
Qy 2000 TCGCAGAGAGCGCTGCTGTTATTTGCAATTCAGAGGCGAATGAAGCGCAAGAGAGAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620
Qy 2060 ATCAGATGGATGATCATATCATCAGGACAGATCAAGGCCCTTCTGCTACGTAGTCTCAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuLeuSerLeuGln 640
Qy 2120 CAGAAGATTCAGGAATTTACTCTGTCCTCGGTGGAAACATGGGTTTCATACAACTCTT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
Qy 2180 CTTAAGGTAACCTCGAAGTCAATTCACACAGAGACTTTGGAAGAACTTCTTCATAAAGAT 2239

Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
Qy 2240 CATGATGGAGATGGCTCTTAAGACCAAAAGAAATGTCCAATAGCATGACACCTAGCCAGAAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
Qy 2300 GTCTGGTACAGAGACTTCATGACACTCATCAACACCCCAATCTCAACACAGATGGATGAG 2359
Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
Qy 2360 TTCTGTGAACAAGTTTGGAAAAGGACCGCAAAACACAGCTCGGCAAGGCCAGGACATACC 2419
Db 721 PheCysGluGlnValTyrLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
Qy 2420 CCAGGAAACAGTAAACAATGGAAGCACTTACAAGAAAATAAGAAAGGTAGAAACAGGAGG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
Qy 2480 ACCCAGCAATTTGAGAGGCGCACCCAGGAGTGTC 2512
Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771
RESULT 3
US-09-060-692-54
; Sequence 54, Application US/09060692
; Patent No. 5935865
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSES: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,692
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-060-692-54
Alignment Scores:
Pred. No.: 0
Score: 771.00
Percent Similarity: 100.00%
Length: 771
Matches: 771
Conservative: 0

Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	86.15%	Indels:	0
DB:	2	Gaps:	0
US-09-774-490-1 (1-2709) x US-09-060-692-54 (1-771)			
QY	200	ATGGGCTGTTAACTAGGATTCCTGCTTTCTGGGAGTATTACTTACAGCAAGACGA	259
DB	1	MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla	20
QY	260	AACATCAAGATGGGAAGAACAAATGTGCCAGGTGAATATATCTCAAGAAATGTTG	319
DB	21	AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu	40
QY	320	GAATCCAAAGTGCATCTTCAATGCTGGCCACAGCTCCAGTTATCATACCTTC	379
DB	41	GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe	60
QY	380	CTTTGGATGAGCAAGGAGTAGGCTGTATGTTGGAGCAAAAGGATCACATATTTTCATTC	439
DB	61	LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe	80
QY	440	GACCTGGTTAATATCAAGATTTTCAAAAGATTGTGTGCCAGTATCTTACACCAAGA	499
DB	81	AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg	100
QY	500	GATGAATCAAGTGGCTGGAAAGACATCTCGAAAGAAATGTCTAAATTTTCATCAAGGTA	559
DB	101	AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal	120
QY	560	CTTAAGGCATATAATCAGACTCACTTGACGCTGTGGAAACGGGGCTTTTCATCCAAT	619
DB	121	LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle	140
QY	620	TSCACTCATTTGAATGGACATCATCTGAGGACAAATATTTTAAAGCTGGAGAACTCA	679
DB	141	CysThrTyrIleGluIleGlyHisIleProGluAspAsnIlePheLysLeuGluAsnSer	160
QY	680	CATTTTGAACCGCGTGGGAAGAGTCCATATGACCTTAAGCTCTCAGACGATCCCTT	739
DB	161	HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu	180
QY	740	TTAATAGATGGAGATTATCTCTGGAACCTGAGCTGATTTTATGGGCGAGACTTTGCT	799
DB	181	LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla	200
QY	800	ATCTTCCGAACCTTGGGCACCAACCAACAGCAGACAGCAGCATGATTCACAGGTGG	859
DB	201	IlePheArgThrLeuGlyHisIleHisIlePheArgThrGluGlnHisAspSerArgTrp	220
QY	860	CTCAATGATCCAAAGTTCATAGTCCCACTCATCTCAGAGAGTGACAACTCTGAAGAT	919
DB	221	LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp	240
QY	920	GACAAAGTATCTTTTCTTCGCTGAAATGCAATAGATGAGAACACTCTGGAAAGCT	979
DB	241	AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla	260
QY	980	ACTCAGCTAGAATAGGTGAGATATCCAAAGATGACTTTGGAGGCGACAGAGTCTGGT	1039
DB	261	ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal	280
QY	1040	ATAATAGCAACACTCTCTCAAGCTGCTGTGATTTCTCAGTCCAGGTCCTCAATGCG	1099
DB	281	AsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly	300
QY	1100	ATTGACACTCATTTTGCATGAACTGAGGATGATTTCTTAATGAATTTAAAGATCCTAAA	1159
DB	301	IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys	320
QY	1160	ATCCAGTTGTATAGGAGTGTTCAGACTTCCAGTACATTTTCAAGGGATCAGCCGTG	1219
DB	321	AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal	340

QY	1220	TGTATGTATAGCATGATGATGTGAGAGGGTGTCTCTGCTCATATGCCACACGGAT	1279
DB	341	CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp	360
QY	1280	GGACCCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTTATCCAGCCGAGAACT	1339
DB	361	GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr	380
QY	1340	TGTCACGCAAAACANTTGGTGGTTTGTACTCTACAAAGGACCTTCTGTATGTATATA	1399
DB	381	CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspValIle	400
QY	1400	ACCTTTGCCAAAGATCATCCAGCCATGTACAAATCCAGTGTTCCTATGAACAATCCCCCA	1459
DB	401	ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro	420
QY	1460	ATAGTGATCAAAACGGAGTAAATATCAATTTACAAATTTCTGTAGACCGAGTGGAT	1519
DB	421	IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp	440
QY	1520	GCAGAGATGCAGATGATGATGTTATGTTATCGGAACAGATGTTGGACCGTCTTAAA	1579
DB	441	AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys	460
QY	1580	GTAAGTTTCAATCTTAAAGGAGACTTGGTATGATTTAGAAAGAGTTCTGCTGGAGAAATG	1639
DB	461	ValValSerIleProLysGluThrTrpTyrAspLeuGluGluValLeuLeuGluMet	480
QY	1640	ACAGTTTTCGGAAACCGACTGCTATTTCAGCAATGAGCTTTCCACTAAGCAGCAACAA	1699
DB	481	ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGlnGln	500
QY	1700	CTATATATTTGGTTCAACGGCTGGGGTGGCCAGCTCCCTTTACACGGGTGTGATATTAC	1759
DB	501	LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr	520
QY	1760	GGGAAACGCTGCTGAGTGTTCCTCGCCCGAGACCTTACTGCTGCTGGATGTTCT	1819
DB	521	GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer	540
QY	1820	GCAATGTTCTCGCTATTTTCCACTGCAAGAGAGACGACAAAGACGACAAAGATATAA	1879
DB	541	AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgArgGlnAspIleArgAsn	560
QY	1880	GGAGACCACTGACTCAGTCTTACAGCTTACACCATGATAATCACCATGCGCCACAGCCCT	1939
DB	561	GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro	580
QY	1940	GAGAGAGATCATCTATGCTGTAGCAATAGTAGCACATTTTGGAAATGCACTCCGAAG	1999
DB	581	GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys	600
QY	2000	TCGCAGAGAGCGTGTGTTATTGGCAATTCAGAGCGGCAATGAAGCGCAAGAGAGAG	2059
DB	601	SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu	620
QY	2060	ATCAGAGTGAATCATATCATCATCAGACAGATCAAGGCCCTTCTGTACGTAGTACAA	2119
DB	621	IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln	640
QY	2120	CAGAAGGATTTCAGCAATTAACCTCTGCCATGCGGTGCAACATGGGTTTCATACAACTCT	2179
DB	641	GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu	660
QY	2180	CTTAAGTAAACCTTGAAGTCAATTGACACAGACATTTTGAAGAAGCTTCTTCAAGAT	2239
DB	661	LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp	680
QY	2240	GATCATGGAGATGGCTCTAGACCAAGAAATGTCCAATAGCATGACACCTACCCAGAAG	2299
DB	681	AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys	700

QY 2300 GTCTGGTACAGAGACTTCATGCACTCATCAACACACCCCAATCTCAACACGATGGATGAG 2359
Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
QY 2360 TTCTGTGACAGAGTTGGAAAGGACCGAAACAACTCGGCAAGCCAGGACATACC 2419
Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
QY 2420 CCAGGGAACAGTAACAAATGGAACACTTACAGAAATAAGAAAGGTAGAAAACAGAGG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
QY 2480 ACCACAGATTGAGAGGACCCAGGAGTGC 2512
Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 4
US-08-833-391-54
; Sequence 54, Application US/08833391
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,391
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,713
; FILING DATE: 13-SEP-1993

ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELETYPE:
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein

US-08-833-391-54
Alignment Scores:
Pred. No.: 0
Score: 771.00
Percent Similarity: 100.00%
Best Local Similarity: 100.00%
Query Match: 86.15%
DB: 3
Gaps: 0
Indels: 0
Mismatch: 0
Conservative: 0
Matches: 771
Length: 771

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QY 260 AACTATCAGAATGGGAAGACAAATGTGCCAAGGTGAAATATCTCAAGAAATGTTG 319
Db 21 AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCAAATATGATACATTTTCAATGGCTTGGCCACAGCTCCAGTATCATACCTTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
QY 380 CTTTGGTATGAGAACGAGTAGGTGTATCTTGGCAAGAGGATCATATTTTCAATTC 439
Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGGTTAATATCAAGGATTTTCAAAAGATTGTGTGGCCAGCTATCTTACACAGAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
QY 500 GATGAATGCACTGGCTGGAAAGACATCTCTGAAGAAATGTCTAATTTTCAATCAAGTA 559
Db 101 AspGluCysLysTrpAlaGlyLysAspLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATATCAAGACTCATTTGTACGCTGTGGAACGGGGCTTTTCATCCAATT 619
Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTACATGAAATTTGGACATCATCTGAGGACATATTTTAACTCGGAGAACTCA 679
Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTGTGAAAACGGCCGTGGGAAGAGTCCATATGACCTTAAGCTCTCAGACGATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGGAGATTTACTCTGGAATCTGAGTGTGATTTTATGGGCGAGACTTGTCT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCCGAACCTCTTGGGCGACCCACCACCAATTCAGGACAGACGACATGATTCAGSTGG 859
Db 201 IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCATATGATCCAAAGTTCATTTAGTCCCACTCATCTCAGAGAGTCAAACTCGAAGAT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATACCTTTTCTTCGTCGAAATGCAATAGATGGAGAACACTCTGGAAAAGCT 979
Db 241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ACTCAGCTAGAAATAGGTGAGATATGCAAGAAATGCTTTGGAGGCGCACAGAGTCTGGTG 1039
Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
QY 1040 AATAATGACACACATTTCTCAAGCTCGTCTGATTTGCTCAGTCCAGGTCCCAATGCGC 1099
Db 281 AsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
QY 1100 ATTGACACTCATTTTGATGAAGTGCAGGATGATTTCTTAATGAATTTTAAAGATCCTAAA 1159
Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
QY 1160 ATCCAGTTGTATATGAGTGTTCAGCTTTTACGACTTCCAGTAACTTTTCAAGGGATCACCCGTG 1219
Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
QY 1220 TGTATGTATAGCATGATGATGTGAGAGGGTGTTCCTTGGTCCATATGCCACAGGAT 1279
Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360
QY 1280 GGACCAACTATCAATGGGTGCTTATCAAGAAAGTCCCTATCCACGGCCAGGAAC 1339

Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
Qy 1340 TGTCACCAACAAATTTGGTGGTTTGGACTCTACAAAGGACCTTCCTGATGATGTTATA 1399
Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValle 400
Qy 1400 ACCTTTGCAGAGTCATCCAGCATGATGACATCAATCCAGTGTTCCTATGACAAATCGCCCA 1459
Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
Qy 1460 ATAGTGATCAAAACCGATGTAATTTATCAATTTACAAATTTGCTAGACCGAGTGGAT 1519
Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValasp 440
Qy 1520 GCAGAGATGCACAGTATGATGTTATGTTATCGGAACAGATGTGGACCGTCTTAA 1579
Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
Qy 1580 GTAGTTTCAATTCCTAAGGACCTGGTATGATTTAGAGAGTTCCTGCGAAGAAATG 1639
Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluGluMet 480
Qy 1640 ACAGTTTTCGGGAACCGACCTGCTATTTACAGCAATGGAGCTTTCACCTAAGCAGCAACA 1699
Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
Qy 1700 CTATATATGTTTCAACGGCTGGGGTTCGCCAGCTCCCTTTACACCGGTGTGATTTAC 1759
Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
Qy 1760 GGGAAAGCGTGCTGACGTGTTGCTCGCCGAGACCTTACTGTGCTGGATGGTCT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
Qy 1820 GCATGTTCTCGCTAATTTTCCACTGCAAGAGACGCAACAGCAAGATATAGAAAT 1879
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgThrArgGlnAspIleArgAsn 560
Qy 1880 GGAGACCACTGACTCACTGTTCAGACTTACACCATGATATACCATGGCCACAGCGCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisGlyHisSerPro 580
Qy 1940 GAAGAGAGATCATCTATGTTGATAGAAATAGTACACATTTTGGATGCGAGTCCGAAG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
Qy 2000 TCGCAGAGAGCGCTGCTATTCGCAATTCAGAGCGCAATAGAGCGCAATAGAGCGAAAGAGAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgAsnGluArgLysGlnGlu 620
Qy 2060 ATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCCTTCGTACGTAGTCTACAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
Qy 2120 CAGAGAGATTCAGGCAATTCCTGCGATCGGTGGAAACATGGGTTTCATCAAACTCTT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
Qy 2180 CTTAAGGTAAACCTCGAAGTCACTTCACACAGAGCATTTGGAAGACTTCTTCATAAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluLeuLeuLeuHisLysAsp 680
Qy 2240 GATGATGGAGATGGCTCTAAGACCAAGAAATGTCCCAATAGCATGACACCTAGCCAGAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
Qy 2300 GTCTGGTACAGAGACTTCATGAGCTCATCAACACCCCAATCTCAACACAGATGATGAG 2359
Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
Qy 2360 TTCTGTGACAAAGTTTGGAAAAGGACCGCAAAACAGCTCGCAAGGCCACGAGCATACC 2419

Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
Qy 2420 CCAGGGAACAGTAACAATGGAAGCATTACAGAAATAAAGAGGTAGAAACAGGAGG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
Qy 2480 ACCCAGCAATTTGAGAGGCGCACCCAGGAGCTGTC 2512
Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771
RESULT 5
US-09-060-610-54
; Sequence 54, Application US/09060610
; Patent No. 6344544
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,610
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/835,268
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-060-610-54
Alignment Scores:
Pred. No.: 0 Length: 771
Score: 771.00 Matches: 771
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 86.15% Indels: 0
DB: 4 Gaps: 0
US-09-774-490-1 (1-2709) x US-09-060-610-54 (1-771)
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Qy 260 AACTATCAGAAATGGGAAGCAATGTGCCAAGCTGAAATTCCTACAAAGAAATGTTG 319

Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
Qy 320 GAATCCAAATGATGATCACTTTCAATGGCTGGCCCAACAGCTCCAGTTATCATCTTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
Qy 380 CTTTGGATGAGGAACGAGTGGCTGTATGTTGGCAAGGATCATATTTTCATTC 439
Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
Qy 440 GACCTGGTTAATCAAGGATTTTCAAAAGATTCTGGCCAGTATCTTACACAGAAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
Qy 500 GATGAATGCAAGTGGCTGGAAAGACATCTGTGAAGAATGCTGAATTTTCATCAAGGTÀ 559
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
Qy 560 CTTAAGGCATATAATCAGACTCACTTGTAGCCCTGTGGAACGGGGCTTTTCATCCAATT 619
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Qy 620 TGCACCTACATGAAATGGACATCCTCGAGACAAATATTTTAAGCTGGAGAACTCA 679
Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
Qy 680 CATTTTGAACCGCTGGGAAGAGTCCATATCACCTTAAGCTGCACAGCATCCCTT 739
Db 161 HisPheGluAsnGlyA-GlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
Qy 740 TTAATAGATGAGAAATTAATCTCTGGAACTGCAGCTGATTTTATGGGGCAGACTTTGCT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyA-GaspPheAla 200
Qy 800 ATCTCCGAATCTTGGCCACACCCATCATAGAGACAGACAGAGCATGATTCAGGTGG 859
Db 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
Qy 860 CTCAATGATCAAAAGTTCAATAGTGGCCACCTCATCTCAGAGAGTGACAAATCCCTGAAGAT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
Qy 920 GACAAAGTATCTTTCTTCGGTGAATTCATAGATGGAGAACACTCTGGAAAGCT 979
Db 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGlyHisSerGlyLysAla 260
Qy 980 ACTCAGCTAGAAATGAGTCAAGATGCAAGAAATGACATTTGGAGGCCACAGAAGTCTGGTG 1039
Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
Qy 1040 AATAAATCGACAACATTCCTCAAGCTCGTGTGATTTGCTCAGTCCAGGTCCAAATGGC 1099
Db 281 AsnLysTrpThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
Qy 1100 ATTGACACTCAATTTTGAATCGAGGATGATTTCTTAATGAATTTAAAGATCCCTAAA 1159
Db 301 IleAspThrHisPheAspGluGlnAspValPheLeuMetAsnPheLysAspProLys 320
Qy 1160 AATCAGCTGTATATGAGTGTTCACGACTTCCAGTAAACATTTTCAAGGATCAGCCGTG 1219
Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
Qy 1220 TGATGATACATGAGTGTGAGAGGTGTTCTTGTGCTCATATGCCACAGGGAT 1279
Db 341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360
Qy 1280 GGACCCCAACTATCAATGGGTCCCTTATCAAGGAAGAGTCCCTTATCCACGCCACGGAAC 1339
Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
Qy 1340 TGTCACACAAACATTTGGTGGTTTGTACTCTCAAGAGGCTTCTGTATGATGTTATA 1399
Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400

Qy 1400 ACCTTTGCAAGAAGTCATCCAGCCATGTACAATCCAGTGTTCCTATGAACAATCGCCCA 1459
Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
Qy 1460 ATAGTGATCAAAACGGATGTAATTTATCAATTTACAAAATTCGTAGACCGAGTGAT 1519
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Qy 1520 GCAGAGATGACAGATGATGTATGTTATCGGAACAGATGTTGGACCGTTCCTTAAA 1579
Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
Qy 1580 GTAGTTTCAATTCCTAAGGAGACTTGTGTATGATTAGAAAGAGTTCCTCTGGAAGAAATG 1639
Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluGluValLeuLeuGluMet 480
Qy 1640 ACAGTTTTTGGGAACCGACTGCTATTTACAGAAATGGAGCTTTCACCTAGACACACAA 1699
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Qy 1700 CTATATATTGGTTCAACGGCTGGGGTTCGCCAGCTCCCTTTACACCGGTGTGATATTAC 1759
Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
Qy 1760 GGGAAAGCGTGTGCTGAGTGTGCTCCCGAGACCTTACTGTGCTGGATGGTGTCT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
Qy 1820 GCATCTTCTCCCTATTTCCCACTGCAAGAGAGCACAAGACAGACAGATATAAGAAAT 1879
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgThrArgGlnAspIleArgAsn 560
Qy 1880 GGAGACCCACTGACTCACTGTTCAGACTTACACCATGATAATCACCATGGCCACAGCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisGlyHisSerPro 580
Qy 1940 GAAGAGAAATCATCTATGCTGTAGAGATAGTACCATTTTGGAAATGACAGTCCGAAG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerThrPheLeuGluCysSerProLys 600
Qy 2000 TCCACAGAGCGCTCGTCTATTGGCAATTCAGAGCGGGAATGAAGAGCGAAAACAGAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgA-GAsnGluGluArgLysGluGlu 620
Qy 2060 ATCAGAGTGATGATCATATCATCAGGACAGATCAGCCCTTCTGTACGTAGTCTACAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
Qy 2120 CAGAAGGATTCAGGCAATTCCTCTCGCATCGGTGGAAACATGGTTCATCAAACTCTT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
Qy 2180 CTTAAGCTAACCTCGAAGTCATTACACAGAGCATTTGGAAAGAACTTCTTCATAAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
Qy 2240 GATGATGGAGTGGCTCTAAGACCAAGAAATGTCCAATAGCATCAGACCTAGCCAGAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
Qy 2300 GTCTGGTACAGAGACTTTCAGCTCATCAACCCCAATCTCAACCATGATGATGAG 2359
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Qy 2360 TTCTGTGAACAATTTGGAAGGACCGAAACAACTCGTCGCAAGAGCCAGGACATACC 2419
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Qy 2420 CCAGGAAACAGTAAACAAATGGAAGCACTTACAAGAAAAATAAGAAAGGTAGAAACAGGAGG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760

QY 2480 ACCACGAAATTTGAGAGGCGCCAGGAGTGC 2512
Db ||||||||||||||||||||||||||||||||||| 771
761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 6
PCT-US94-10151A-54
; Sequence 54, Application PC/TUS9410151A
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESS: FLEHR HOEBACH TEST ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10151A
; FILING DATE: 13-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: FP-58750-PC/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299 FHT UR
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US94-10151A-54

Alignment Scores:
Pred. No.: 0 Length: 771
Score: 771.00 Matches: 771
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 86.15% Indels: 0
DB: 5 Gaps: 0

US-09-774-490-1 (1-2709) x PCT-US94-10151A-54 (1-771)

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QY 260 AACTATCAGATGGGAGCAACAAATGTGCCAGGCTGAATATCTCTACAAAGAAATGTG 319
Db 21 AsnTyrGluAsnGlyLysAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCAAATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCATACCTTC 379
Db 41 GluSerAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
QY 380 CTTTGGATCAGGAACGGAGTAGGCTGTATGTGGAGCAAGGATCACAATTTTCATTC 439
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QY 440 GACCTGGTAAATATCAAGGATTTTCAAGATGTGTGGCCAGTATCTTACACCAAGAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100

QY 500 GATGAATGCAAGTGGCTGGAAGAGCATCTCTGAAAGAAATGTCTAATTTTCAAGGTA 559
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101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATTAATCAGACTCACTTGTAGCTGTGGAAACGGGGCTTTTCAATTC 619
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QY 620 TGCACCTACATTCGAAATTTGACATCATCTCTGAGGACAATATTTTAACTGGAGAACTCA 679
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141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
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QY 1160 AATCCAGTTGTATATGGAGTGTTCAGACTTCCAGTAAACATTTTCAAGGGATCAGCGCTG 1219
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QY 1280 GGACCCCACTATCAATGGGTGCTTATCAAGGAGAGTCCCTTATCCAGCCGAGGAACT 1339
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QY 1340 TGTCACAGCAAAACATTTGGTGGTGTTCAGTCTACAAAGGACCTTCTGTATGATGTATA 1399
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Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluGluValLeuLeuGluMet 480
Qy 1640 ACAGTTTTCGGACCGACTGCTATTTCCAGCAATGGAGCTTTCACCTAAGACGACAA 1699
Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
Qy 1700 CTATATATTGGTCAACGGCTGGGTTGCCAGCTCCCTTTACACCGGTGTGATATTAC 1759
Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
Qy 1760 GGGAAAGCGTGTGCTGAGTGTGCTCCCGAGACCTTACTGCTGGTGGATGTTCT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
Qy 1820 GCATGTTCTCGCTATTTCCCACTGCCAAGAGACGCAAGACGACAGATATAAGAAAT 1879
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560
Qy 1880 GGAGACCCACTGACTCTGCTTCTAGACTTACACCATGATATACCATGGCCAGCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisGlyHisSerPro 580
Qy 1940 CAAGAGCAATCATCTATGGTGTAGAAATAGTAGCAGCATTTTGGATGCGAGCCGAAG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
Qy 2000 TCGCAGAGCGCTGGTCTATTGGCAATTCAGAGGGGAAATGAAGAGCGAAAGAAGAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620
Qy 2060 ATCAGAGTGGATGATCATATCATCAGCAGCATCAGGCTTCTGCTACGTAGTCTACAA 2119
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Qy 2120 CAGAAGGATTTCAGGCAATTAACCTCTGCCATCGGTGGAACATGGGTTTCATACAACTCTT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
Qy 2180 CTTAAGTTAACCTGGAGTCAATTCAGCAGAGCATTTGGAGAACTTCTTCATAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuHisLysAsp 680
Qy 2240 GATGATGAGATGGCTCTAAGACCAAGAAATGTCCATAGCATGACACCTAGCGCAAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
Qy 2300 GTCTGGTACAGACTTCATGAGCTCATCAACACCCCAATCTCAACAGATGGATGAG 2359
Db 701 ValTyrTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
Qy 2360 TTCTGTGAACAGTTTGGAAAGGACCGAAAAACAACGTCCGCAAGCCAGGACATACC 2419
Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
Qy 2420 CCAGGGAACAGTAAACAATGGAAGCACTTACAAGAAATAGAAGGTAGAAACAGGAGG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
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Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771
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RESULT 7

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US-08-556-422A-3
; Sequence 3, Application US/08556422A
; Patent No. 6576754
; GENERAL INFORMATION:
; APPLICANT: HALL, Kathryn T.
; APPLICANT: FREEMAN, Gordon J.
; APPLICANT: SCHULTZE, Joachim L.
; APPLICANT: BOUSSIOTIS, Vassiliki
; APPLICANT: NADLER, Lee M.
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; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DFN-005CPA2
; CURRENT APPLICATION NUMBER: US/08/556,422A
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-556-422A-3

Alignment Scores:
Pred. No.: 0 Length: 655
Score: 655.00 Matches: 655
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 73.18% Indels: 0
DB: 4 Gaps: 0
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US-09-774-490-1 (1-2709) x US-08-556-422A-3 (1-655)

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Db 1 MetGlyTyrLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
Qy 260 AACTATCAAGATGGGAACAATGTCGCAAGCTGAAATATCTACAAAGAAATGTTG 319
Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
Qy 320 GAATCAACAATGTGATCACATTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATACCTTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
Qy 380 CTTTGTGATGAGGAACGAGTAGGCTGTATGTTGGAGCAAAAGGATCACATATTTTCATTC 439
Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
Qy 440 GACCTGTTTAAATATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACACCAAGAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
Qy 500 GATGAATCAAGTGGCTGGAAAAGACATCTCTGAAAGAATGTGCTAATTTTCATCAGATA 559
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
Qy 560 CTTAAGGCATATAATCAGACTCACCTGTACGCTCTGGAACGGGGCTTTTCATCCAATT 619
Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
Qy 620 TGCACCTACATTGAAATTTGGACATCATCTGAGGACAATATTTTAACTGGAGAACTCA 679
Db 141 CysThrTyrIleGluIleGlyHisProGluAspAsnIlePheLysLeuGluAsnSer 160
Qy 680 CATTTTGAACACGGCGTGGGAGAGTCCATATGACCTTACCTAGCTCTCAGACATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
Qy 740 TTAATAGATGGAGAATTATACTCTCGAACTGCAGCTGATTTTATGGGCGAGACTTCTCT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
Qy 800 ATCTTCGGAACCTTTGGGCAACCCACCACCATCAGACAGACAGACATGATTCAGGTTG 859
Db 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
Qy 860 CTCATATGATCCAAAGTTTCATTAGTGTCCCACTCTCATCTCAGAGAGTGACAATCTCTGAAGAT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
Qy 920 GACAAAGTATATCTTTTCTTCGTTGAAAATGCAATAGATGAGAAACATCTCTGGAAGCT 979
Db 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
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QY 980 ACTCAGCTAGATAGTCAGATATGCAAGAAATGACTTTGGAGGGCACAGAAGTCTGGT 1039
Db 261 ThrHisAlaAaGllleGlyGlnlleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
QY 1040 AATAAATGGACAACATTCCTCAAGCTCGTCTGATTTGCTCAGTGCAGGTCGAATGGC 1099
Db 281 AsnLysTrpThrPheLeuLeuAlaArgLeuileCysSerValProGlyProAsnGly 300
QY 1100 ATTGACACTCATTTTGATGAACTGCAGGATGATATCTTAATGAACCTTTAAAGATCCTAAA 1159
Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProlys 320
QY 1160 AATCCAGTTGATATGGAGTGTTCAGCATTCCTAGTAACATTTCAAGGGATCAGCCGTG 1219
Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
QY 1220 TGTATGTATACATGATGATGTCAGAGGGTTCCTGTCATATGCCATATGCCACAGGAT 1279
Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360
QY 1280 GGACCCAACTATCAATGGTGCCTTTATCAAGGAAGAGTCCCTATCCACGGCCAGGAAC 1339
Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
QY 1340 TGTCCACAAACATTTGGTGGTTCCTACTCTCAAGAGACCTTCCTGATGATTTATA 1399
Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspValIle 400
QY 1400 ACCTTTGCAAGAGTCATCCAGCCATGTACAACTCAGTGTTCCTATCAACAAATCGCCCA 1459
Db 401 ThrPheAlaAaGSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
QY 1460 ATAGTGATCAAAACGGATGTAATATCAATTTACAAATTCGATAGCCGAGTGGAT 1519
Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
QY 1520 CGAGAAGATGACATGATGATGTTATCGGAACAGATGTGGACCGTCTTAA 1579
Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
QY 1580 GTAGTTCAATTCCTAAGGACATTTGATGATTTAGAAAGGTTCTGCTGGAAGAAATG 1639
Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluGluMet 480
QY 1640 ACAGTTTTCGGGAACCACTGCTATTTCCAGCAATGGAGCTTCCACTAAGCAGCAACA 1699
Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
QY 1700 CTATATATTGGTTCAACGGCTGGGGTTCCTCCAGCTCCCTTTACACCGGTGTGATATTAC 1759
Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
QY 1760 GGAAGAAGCGTGTGATGATGTTGCTCGCCGAGACCTTACTGTGCTGGGATGGTTCT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
QY 1820 GCATGTTCTCGCTATTTTCCCACTCAAGAGACCCCAAGACGACAGATATAGAAAT 1879
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgThrArgGlnAspIleArgAsn 560
QY 1880 GGAGACCCACTGACTCAGTGTTCAGACTTACACCATGATAATCACCATGGCCACAGCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisHisGlyHisSerPro 580
QY 1940 GAAGAGAGATCATCTATGCTGTAGAGATAGTACACATTTTGGATGAGTCCGAG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProlys 600
QY 2000 TGCAGAGAGCCCTGCTTATGGCAATTCAGAGCGCAATGAGAGCGAAAGAGAGAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgAsnGluGluArgLysGluGlu 620

QY 2060 ATCAGAGTCGATCATATCATATCATAGGACAGATCAAGGCTTCTGCTAGTGTCTACAA 2119
Db 621 IleArgValAspAspHisIlelleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
QY 2120 CAGAAGGATTCAGGCAATTACCTCTGCCATGCGTGGGAACATGGG 2164
Db 641 GlnLysAspSerGlyAsnIlyrLeuLysHisAlaValGluHisGly 655
RESULT 8
US-08-136-922-2
: Sequence 2, Application US/08136922
: Patent No. 5416197
: GENERAL INFORMATION:
: APPLICANT: Reper, Jonathan A.
: APPLICANT: Luo, Yuling
: TITLE OF INVENTION: Compositions Which Regulate Neural
: TITLE OF INVENTION: Regeneration and Methods of Making and Using the Same
: NUMBER OF SEQUENCES: 2
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
: STREET: One Liberty Place
: CITY: Philadelphia
: STATE: PA
: COUNTRY: USA
: ZIP: 19103
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/136,922
: FILING DATE:
: CLASSIFICATION: 435
: ATTORNEY/AGENT INFORMATION:
: NAME: Deluca, Mark
: REGISTRATION NUMBER: 33,229
: REFERENCE/DOCKET NUMBER: UPN-1428
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 215-568-3100
: TELEFAX: 215-568-3439
: INFORMATION FOR SEQ ID NO: 2:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 477 amino acids
: TYPE: amino acid
: TOPOLOGY: linear
: MOLECULE TYPE: protein
US-08-136-922-2
Alignment Scores:
Pred. No.: 0 Length: 477
Score: 434.00 Matches: 434
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 48.49% Indels: 0
DB: 1 Gaps: 0
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QY 905 GACAATCCTCAAGATGACAAAGTATACTTTTCTTCGTGMAAATGCAATAGATGAGAA 964
Db 4 AspAsnProGluAspAspLysValTyrPhePheArgGluAsnAlaIleAspGlyGlu 23
QY 965 CACTCTGGAAAAGCTACTCAGCTAGATAGGTGACATATGCAAGAATGACTTTGGAGGG 1024
Db 24 HisSerGlyLysAlaThrHisAlaAaGllleGlyGlnlleCysLysAsnAspPheGlyGly 43
QY 1025 CACAGAAGTCTGGTGAATAAATGCAACAATTCCTCAAGCTCTGATTTGCTCAGTG 1084
Db 44 HisArgSerLeuValAsnLysTrpThrPheLeuLysAlaArgLeuileCysSerVal 63
QY 1085 CCAGGTCCTCAATGGCATTGACACTCATTTTGTATGATGAACATGTCAGGATGTATTCTTCAATGAAC 1144

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Db      64  ProGlyProAsnGlyIleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsn 83
      1145  TTTAAAGATCCTAAATCCAGTGTATATAGAGTGTTCAGCTCCAGTACATTTTC 1204
Db      84  PheLysaspProLysAsnProValValTyGlyValPheThrThrSerSerAsnIlePhe 103
      1205  AAGGATCAGCGGTGTGTATATAGCATGATGATGAGAGGGTGTTCCTTGTCCTCA 1264
Db     104  LysGlySerAlaValCysMetTySerMetSerAspValargValPheLeuGlyPro 123
      1265  TATGCCACAGGATGAGCCCACTATCATATGGTGTCTTATCAGGAAGATCCCTAT 1324
Db     124  TyrAlaHisArgAspGlyProAsnTyGlnTrpValProTyGlnGlyArgValProTy 143
      1325  CCAGGCCAGAACTGTGCCAGCAAAACATTTGGTGGTTTGTACTCTACAAAGGACCTT 1384
Db     144  ProArgProGlyThrCysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeu 163
      1385  CTTGATGATGTTAACTTTGCAAGAGTCAATCCAGCCATGTACATCCAGTGTTCCT 1444
Db     164  ProAspValIleThrPheAlaArgSerHisProAlaMetTyAsnProValPhePro 183
      1445  ATGACATCCCAATAGTATCAAAACGATGTAATATCAATTTACAAATTTGTC 1504
Db     184  MetAsnAsnArgProIleValIleLysThrAspValAsnTyGlnPheThrGlnIleVal 203
      1505  GTAGACCGAGTGGATGAGAGATGCGAGTATGATGTTATCGGAACAGATGTT 1564
Db     204  ValAspArgValAspAlaGluAspGlyGlnTyAspValMetPheIleGlyThrAspVal 223
      1565  GGGACCGTCTTAAGTAGTTTCAATTCCTAAGAGACTGGTATGATGATGATGAGAGTT 1624
Db     224  GlyThrValLeuLysValValSerIleProLysGluThrTrpTyAspLeuGluGluVal 243
      1625  CTGTCGGAAGAAATGACAGTGTTCGGAACCGAGTCTATTTTCCAGCAATGCGACTTCC 1684
Db     244  LeuLeuGluGluMetThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSer 263
      1685  ACTAAGCAGCAACATATATATGTTTCAAGCGCTGGGTGCGCCAGCTCCCTTTACAC 1744
Db     264  ThrLysGlnGlnLeuTyIleGlySerThrAlaGlyValAlaGlnLeuProLeuHis 283
      1745  CGGTGTATATTTACGGAAGAGCTGTCTCAGAGTGTTCCTCGCCGAGAGCCCTTACTGT 1804
Db     284  ArgCysAspIleTyGlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyCys 303
      1805  GCTTGGGATGTTCTGCATGTTCTCGCTATTTTCCACTGCAAGAGACGCAAGACGA 1864
Db     304  AlaTrpAspGlySerAlaCysSerArgTyPheProThrAlaLysArgArgThrArg 323
      1865  CARGATATAAGAAATGAGAGCCCTGCTCAGTCTGTTCCAGCTTACACCATGATATCAC 1924
Db     324  GlnAspIleArgAsnGlyAspProLeuThrHisCysSerAspLeuHisAspAsnHis 343
      1925  CATGCCACAGCCCTGAGAGAGATCATCATCATCATCATCATCATCATCATCATCAT 1984
Db     344  HisGlyHisSerProGluGluArgIleIleTyGlyValGluAsnSerSerThrPheLeu 363
      1985  GAATGCACTCGAAGTCCAGAGAGCGGTGTCTATTTGGCAATTCAGAGCGCAATGAA 2044
Db     364  GluCysSerProLysSerGlnArgAlaLeuValTyTrpGlnPheGlnArgArgAsnGlu 383
      2045  CAGCGAAAGAGAGATCAGAGTGGATCATCATCATCATCATCATCATCATCATCAT 2104
Db     384  GluArgLysGluGluIleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeu 403
      2105  CTACGTAGTCTACAAACAGAGAGATTCAGCAATTTACCTCTGCGCTGCGGTGGACATGG 2164
Db     404  LeuArgSerLeuGlnGlnLysAspSerGlyAsnTyLeuCysHisAlaValGluHisGly 423
      2165  TTACATCAAACTCTTCTTAAAGTAACTGCAAGTCAATGAC 2206

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Db      424  PheIleGlnThrLeuLeuLysValThrLeuGluValIleAsp 437
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      ; Sequence 1, Application US/09308179B
      ; Patent No. 6436689
      ; GENERAL INFORMATION:
      ; APPLICANT: INAGAKI, Shinobu
      ; APPLICANT: FURUYAMA, Tatsuo
      ; TITLE OF INVENTION: NOVEL SEMAPHORIN GENES (I)
      ; FILE REFERENCE: 0020-4562P
      ; CURRENT APPLICATION NUMBER: US/09/308,179B
      ; CURRENT FILING DATE: 1999-05-14
      ; PRIOR APPLICATION NUMBER: PCT/JP97/04111
      ; PRIOR FILING DATE: 1997-11-12
      ; PRIOR APPLICATION NUMBER: JAPAN 321068/1996
      ; PRIOR FILING DATE: 1996-11-15
      ; NUMBER OF SEQ ID NOS: 4
      ; SOFTWARE: PatentIn Ver. 2.1
      ; SEQ ID NO 1
      ; LENGTH: 775
      ; TYPE: PRT
      ; ORGANISM: Mus sp.
      US-09-308-179B-1
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      Pred. No.: 0.000703 Length: 775
      Score: 13.00 Matches: 13
      Percent Similarity: 100.00% Conservative: 0
      Best Local Similarity: 100.00% Mismatches: 0
      Query Match: 1.45% Indels: 0
      DB: 4 Gaps: 0
      US-09-774-490-1 (1-2709) x US-09-308-179B-1 (1-775)
      QY      1778  TGTTCCTCGCCGAGACCCCTTACTGTCTGGATGGT 1816
      Db      529  CysCysLeuAlaArgAspProTyCysAlaTrpAspGly 541
      RESULT 10
      US-09-041-236-4
      ; Sequence 4, Application US/09041236
      ; Patent No. 6225285
      ; GENERAL INFORMATION:
      ; APPLICANT: Luo, Yuling
      ; APPLICANT: Xiomei, Xu
      ; TITLE OF INVENTION: Semaphorin KI
      ; NUMBER OF SEQUENCES: 4
      ; CORRESPONDENCE ADDRESS:
      ; ADDRESSER: SCIENCE & TECHNOLOGY LAW GROUP
      ; STREET: 75 DENISE DRIVE
      ; CITY: HILLSBOROUGH
      ; STATE: CALIFORNIA
      ; COUNTRY: USA
      ; ZIP: 94010
      ; COMPUTER READABLE FORM:
      ; MEDIUM TYPE: Floppy disk
      ; COMPUTER: IBM PC compatible
      ; OPERATING SYSTEM: PC-DOS/MS-DOS
      ; SOFTWARE: PatentIn Release #1.0, Version #1.30
      ; CURRENT APPLICATION DATA:
      ; - APPLICATION NUMBER: US/09/041,236
      ; FILING DATE: March 11, 1998
      ; CLASSIFICATION: 514
      ; ATTORNEY/AGENT INFORMATION:
      ; NAME: OSMAN, RICHARD A
      ; REGISTRATION NUMBER: 36,627
      ; REFERENCE/DOCKET NUMBER: EXEL98-001
      ; TELECOMMUNICATION INFORMATION:
      ; TELEPHONE: (650) 343-4341
      ; TELEFAX: (650) 343-4342
      ; INFORMATION FOR SEQ ID NO: 4:
      ; SEQUENCE CHARACTERISTICS:

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/ LENGTH: 606 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
US-09-041-236-4

Alignment Scores:
Pred. No.: 0.566 Length: 606
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.12% Indels: 0
DB: 3 Gaps: 0

US-09-774-490-1 (1-2709) x US-09-041-236-4 (1-606)
QY 1043 AAATGACAACTTCTCTCAAGCTGCTG 1072
Db 255 LysTrpThrPheLeuLysAlaArgLeu 264

RESULT 11
US-09-771-467C-4
/ Sequence 4, Application US/09771467C
/ Patent No. 6583277
/ GENERAL INFORMATION:
/ APPLICANT: Luo, Yuling
/ TITLE OF INVENTION: Semaphorin K1 Polypeptides
/ NUMBER OF SEQUENCES: 4
/ CORRESPONDENCE ADDRESS:
/ ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
/ STREET: 75 DENISE DRIVE
/ CITY: HILLSBOROUGH
/ STATE: CALIFORNIA
/ COUNTRY: USA
/ ZIP: 94010
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Floppy disk
/ OPERATING SYSTEM: PC-DOS/MS-DOS
/ SOFTWARE: Patent Release #1.0, Version #1.30
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/771,467C
/ FILING DATE: 26-Jan-2001
/ CLASSIFICATION: <Unknown>
/ ATTORNEY/AGENT INFORMATION:
/ NAME: OSMAN, RICHARD A
/ REGISTRATION NUMBER: 36,627
/ REFERENCE/DOCKET NUMBER: EXEL98-001
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: (650) 343-4341
/ TELEFAX: (650) 343-4342
/ INFORMATION FOR SEQ ID NO: 4:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 606 amino acids
/ TYPE: amino acid
/ TOPOLOGY: linear
/ MOLECULE TYPE: protein
/ SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-771-467C-4

Alignment Scores:
Pred. No.: 0.566 Length: 606
Score: 10.00 Matches: 10
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.12% Indels: 0
DB: 4 Gaps: 0

US-09-774-490-1 (1-2709) x US-09-771-467C-4 (1-606)
QY 1043 AAATGACAACTTCTCTCAAGCTGCTG 1072
Db 255 LysTrpThrPheLeuLysAlaArgLeu 264
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Db 255 LysTrpThrPheLeuLysAlaArgLeu 264

RESULT 12
US-09-341-461-34
/ Sequence 34, Application US/09341461
/ Patent No. 6586389
/ GENERAL INFORMATION:
/ APPLICANT: Hammond, Timothy G.
/ APPLICANT: Verroust, Pierre J.
/ TITLE OF INVENTION: Cubilin Protein, DNA Sequences Encoding Cubilin
/ TITLE OF INVENTION: and Uses Thereof
/ FILE REFERENCE: D6148
/ CURRENT APPLICATION NUMBER: US/09/341,461
/ CURRENT FILING DATE: 2000-07-20
/ PRIOR APPLICATION NUMBER: PCI/US99/01259
/ PRIOR FILING DATE: 1999-01-21
/ NUMBER OF SEQ ID NOS: 40
/ SEQ ID NO 34
/ LENGTH: 112
/ TYPE: PRT
/ ORGANISM: human
/ FEATURE:
/ OTHER INFORMATION: amino acid sequence of C1s CUB1 domain
US-09-341-461-34

Alignment Scores:
Pred. No.: 6.39 Length: 112
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.03% Indels: 0
DB: 4 Gaps: 0

US-09-774-490-1 (1-2709) x US-09-341-461-34 (1-112)
QY 151 TTGTGGCGCCAGAGAGTTCAACAAT 125
Db 67 LeuCysGlyGlnArgSerSerAsnAsn 75

RESULT 13
US-08-556-422A-6
/ Sequence 6, Application US/08556422A
/ Patent No. 6576754
/ GENERAL INFORMATION:
/ APPLICANT: HALL, Kathryn T.
/ APPLICANT: FREEMAN, Gordon J.
/ APPLICANT: SCHULTZE Joachim L.
/ APPLICANT: BOUSSETIOTIS, Vassiliki
/ APPLICANT: NADLER, Lee M.
/ TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
/ FILE REFERENCE: DFN-005CFA2
/ CURRENT APPLICATION NUMBER: US/08/556,422A
/ CURRENT FILING DATE: 1995-11-09
/ NUMBER OF SEQ ID NOS: 7
/ SOFTWARE: FastSeq for Windows Version 4.0
/ SEQ ID NO 6
/ LENGTH: 295
/ TYPE: PRT
/ ORGANISM: Gallus gallus
US-08-556-422A-6

Alignment Scores:
Pred. No.: 5.68 Length: 295
Score: 9.00 Matches: 9
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 1.01% Indels: 0
DB: 4 Gaps: 0

US-09-774-490-1 (1-2709) x US-08-556-422A-6 (1-295)
QY 1784 CTGCGCCGAGACCTTACTGTGTTGG 1810
Db 1784 CTGCGCCGAGACCTTACTGTGTTGG 1810
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Db      287 LeuAlaArgAspProTyrCysAlaTrp 295
RESULT 14
US-08-556-422A-7
; Sequence 7, Application US/08556422A
; Patent No. 6576754
; GENERAL INFORMATION:
; APPLICANT: HALL, Kathryn T.
; APPLICANT: FREEMAN, Gordon J.
; APPLICANT: SCHULTZE, Joachim L.
; APPLICANT: BOUSSIOTIS, Vassiliki
; APPLICANT: NADLER, Lee M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DFN-005CPA2
; CURRENT APPLICATION NUMBER: US/08/556,422A
; CURRENT FILING DATE: 1995-11-09
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 7
; LENGTH: 425
; TYPE: PRT
; ORGANISM: Homo sapiens
US-08-556-422A-7

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Pred. No.:      5.44      Length:      425
Score:          9.00      Matches:      9
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Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      1.01%      Indels:      0
DB:               4      Gaps:      0

US-09-774-490-1 (1-2709) x US-08-556-422A-7 (1-425)
QY      1055 TTCTCAAGCTCGTCTGATTGCTCA 1081
Db      104 PheLeuLysAlaArgLeuIleCysSer 112

RESULT 15
US-08-556-422A-4
; Sequence 4, Application US/08556422A
; Patent No. 6576754
; GENERAL INFORMATION:
; APPLICANT: HALL, Kathryn T.
; APPLICANT: FREEMAN, Gordon J.
; APPLICANT: SCHULTZE, Joachim L.
; APPLICANT: BOUSSIOTIS, Vassiliki
; APPLICANT: NADLER, Lee M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DFN-005CPA2
; CURRENT APPLICATION NUMBER: US/08/556,422A
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 607
; TYPE: PRT
; ORGANISM: Mus musculus
US-08-556-422A-4

Alignment Scores:
Pred. No.:      5.21      Length:      607
Score:          9.00      Matches:      9
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:      1.01%      Indels:      0
DB:               4      Gaps:      0

US-09-774-490-1 (1-2709) x US-08-556-422A-4 (1-607)
QY      1784 CTCGCCGAGACCTTACTGCTTGG 1810
Db      483 LeuAlaArgAspProTyrCysAlaTrp 491
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12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:
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19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2709	100.0	2709	9	US-09-774-490-1
2	2517	92.9	2848	15	US-10-247-671-83
3	2508	92.6	2530	15	US-10-097-240-283
4	2508	92.6	2530	15	US-10-262-538-9
5	2508	92.6	2601	15	US-10-067-632-53
6	405	15.0	456	9	US-09-864-761-3092
7	303	11.2	354	9	US-09-922-217-736
8	303	11.2	354	9	US-09-833-263-736
9	303	11.2	354	14	US-10-025-380-736
10	292	10.8	496	9	US-09-864-761-1444
11	161	5.9	164	15	US-10-029-386-18184
12	161	5.9	591	15	US-10-029-386-4484
13	160	5.9	172	9	US-09-864-761-27943
14	160	5.9	191	15	US-10-029-386-16491

C	15	160	5.9	484	9	US-09-864-761-11363	Sequence 11363, A
	16	160	5.9	526	15	US-10-029-386-2791	Sequence 2791, Ap
	17	144	5.3	446	9	US-09-864-761-11810	Sequence 11810, A
	18	123	4.5	123	9	US-09-864-761-28381	Sequence 28381, A
	19	122	4.5	456	9	US-09-864-761-6056	Sequence 6056, Ap
C	20	101	3.7	101	9	US-09-864-761-22893	Sequence 22893, A
	21	71	2.6	2137	9	US-09-774-490-6	Sequence 6, Appli
	22	67	2.5	520	13	US-10-027-632-238542	Sequence 238542,
	23	67	2.5	520	13	US-10-027-632-238543	Sequence 238543,
	24	67	2.5	520	16	US-10-027-632-238542	Sequence 238542,
	25	67	2.5	520	16	US-10-027-632-238543	Sequence 238543,
	26	60	2.2	60	10	US-09-908-975-15846	Sequence 15846, A
	27	50	1.8	50	16	US-10-131-827-4731	Sequence 4731, Ap
	28	31	1.1	4661	9	US-09-897-006-10	Sequence 10, Appl
C	29	31	1.1	4661	10	US-09-897-511A-10	Sequence 10, Appl
	30	31	1.1	4661	13	US-10-397-079-10	Sequence 10, Appl
	31	31	1.1	7160	8	US-08-786-531B-5	Sequence 5, Appli
	32	31	1.1	7235	8	US-08-786-531B-6	Sequence 6, Appli
	33	29	1.1	29	17	US-10-687-241-7	Sequence 7, Appli
	34	26	1.0	1313	9	US-09-728-422-1	Sequence 1, Appli
C	35	25	0.9	25	17	US-10-687-241-2	Sequence 2, Appli
	36	25	0.9	1400	9	US-09-774-490-5	Sequence 5, Appli
	37	24	0.9	24	17	US-10-687-241-1	Sequence 1, Appli
	38	24	0.9	485	10	US-09-814-353-12826	Sequence 12826, A
	39	24	0.9	665	13	US-10-424-599-82082	Sequence 82082, A
	40	24	0.9	1082	10	US-09-814-353-19094	Sequence 19094, A
	41	23	0.8	29	17	US-10-687-241-5	Sequence 5, Appli
C	42	23	0.8	175	13	US-09-990-747-24	Sequence 24, Appl
	43	23	0.8	240	13	US-09-990-747-27	Sequence 27, Appl
C	44	23	0.8	287	13	US-09-990-747-18	Sequence 18, Appl
	45	23	0.8	335	13	US-09-990-747-26	Sequence 26, Appl

ALIGNMENTS

RESULT 1
US-09-774-490-1
; Sequence 1, Application US/09774490
; Patent No. US20010034332A1
; GENERAL INFORMATION:
; APPLICANT: Jhn, Shengfang
; TITLE OF INVENTION: RESISTANCE SEQUENCES AND USES THEREOF
; FILE REFERENCE: 07334-138001
; CURRENT APPLICATION NUMBER: US/09/774,490
; CURRENT FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: US 60/179,191
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-774-490-1

Query Match	100.0%;	Score	2709;	DB	9;	Length	2709;
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Gaps	0;						
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Db	61	ACCCACGGTCGGGAGTAGGTGAGCTCGCCTGTCTCCCATTTGTACGCCAGTCTATTT	120				
QY	121	CCAGATTGTTTGAATTTCTTGGCCGCAATACAGGAGGAGACTAAGCAGCAAGG	180				
Db	121	CCAGATTGTTTGAATTTCTTGGCCGCAATACAGGAGGAGACTAAGCAGCAAGG	180				
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421 Qy GGATCACATATTTTCATTCGACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTGTGCC 480
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1201 Db TTTCAAGGGATCAGCGCTGTATGATAGCATGAGTGTGAGAGGGGTGTTCTTTGG 1260
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1921 Qy TCACCTGGCCACAGCCCTGAGAGAGAACTATCTATGTTGTAGAGAAATAGTAGCACAT 1980
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RESULT 2
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; Sequence 83, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov
; APPLICANT: Porter, Gordon, J.
; APPLICANT: Kaber, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; PRIOR FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,784
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL Program
; SEQ ID NO 83
; LENGTH: 2848
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 1930967CB1
US-10-247-671-83

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 489 GAACTACATTTTGAACACGGCCGTGGGAAGAGTCCATATGACCTTAAGCTGCTGACAGC 548
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	AGAAATGACAGTTTTTTTGGGAAACCGACTGCTATTTTCAGCAATGGAGCTTTCCACTAAGCA	1692
1449	AGAAATGACAGTTTTTTTGGGAAACCGACTGCTATTTTCAGCAATGGAGCTTTCCACTAAGCA	1508
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	GCAACCACTATATATTTGGTTTCAACGGGTGGGGTTGCCAGCTCCCTTTTACACCGGTGTGA	1568
	TATTTACGGGAAAGCGTGTGCTCAGTGTGCTCTCGCCCGAGACCCCTTACTGTGCTTTGGGA	1812
1569	TATTTACGGGAAAGCGTGTGCTCAGTGTGCTCTCGCCCGAGACCCCTTACTGTGCTTTGGGA	1628
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1689	AAGAAATGGAGACCCACTGACTCACTGTTTCAGACTTACACCAATGATTAATCACCATGGCCA	1748
QY	CAGCCCTGAGAGAGATCATCTATGGTGTAGAGAAATGATPAGCACATTTTTTGGAAATGCGAG	1992
	CAGCCCTGAGAGAGATCATCTATGGTGTAGAGAAATGATPAGCACATTTTTTGGAAATGCGAG	1808
	TCGGAAGTCCGAGAGACGCTGTGTTTATTTGGCAATTTCCAGAGGCGAAATGAAGAGCGAAA	2052
1809	TCGGAAGTCCGAGAGACGCTGTGTTTATTTGGCAATTTCCAGAGGCGAAATGAAGAGCGAAA	1868
QY	AGAAAGATCAGAGTGGATGATCATATCATTCAGGACAGATCAAGGCTTCTGTACTGCTAG	2112
	AGAAAGATCAGAGTGGATGATCATATCATTCAGGACAGATCAAGGCTTCTGTACTGCTAG	2112
	AGAAAGATCAGAGTGGATGATCATATCATTCAGGACAGATCAAGGCTTCTGTACTGCTAG	1928
2113	TCCTACACAGAGGATTCAGGCAATTAACCTCTGCCATGCGGTGGAAACATGGGTTCATACA	2172
DQ	TCCTACACAGAGGATTCAGGCAATTAACCTCTGCCATGCGGTGGAAACATGGGTTCATACA	1968
	AACCTCTTTCTTAAGGTAAACCTTGAAGTCAATTGACACAGAGCATTTGGAAAGAACTTCTTCA	2048
	AACCTCTTTCTTAAGGTAAACCTTGAAGTCAATTGACACAGAGCATTTGGAAAGAACTTCTTCA	2048
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2289	CAGAGGACCCACGAAATTTGAGAGGGCACCCAGAGTGTCTGAGCTGCATTAACCTCTAGA	2348
QY	AACCTCAACAAAGTAGAAAATTGCGCTTACAAATTAACCTGGAAAAACAAATGCAATATACAT	2592
	AACCTCAACAAAGTAGAAAATTGCGCTTACAAATTAACCTGGAAAAACAAATGCAATATACAT	2408
	GAACTTTTTTCATGCGCAATTATGTCGATGTTTTTCAATGGTGGGAAATTCAGCTGAGTTCCA	2652
2409	GAACTTTTTTCATGCGCAATTATGTCGATGTTTTTCAATGGTGGGAAATTCAGCTGAGTTCCA	2468

QY	433	TTTCAATCGACCTGGTTAATATCATCAGGAATTTTCAAAAGATTTGTGTGGCCAGTATCTTACAC	492
Db	249	TTTCAATCGACCTGGTTAATATCAAGGAATTTTCAAAAGATTTGTGTGGCCAGTATCTTACAC	308
QY	493	CAGAAGAGATCAATGCAAGTGGCTGGAAAGACATCTGAAAGATGTGCTAATTTTCAT	552
Db	309	CAGAAGAGATCAATGCAAGTGGCTGGAAAGACATCTGAAAGATGTGCTAATTTTCAT	368
QY	553	CAAGGTACTTAAGGCATATAATACAGACTCACTTGTACGCCGTGTGGAAACGGGGGCTTTTCA	612
Db	369	CAAGGTACTTAAGGCATATAATACAGACTCACTTGTACGCCGTGTGGAAACGGGGGCTTTTCA	428
QY	613	TCCAAATTTGCACCTACATTTGAAATTTGGACATCATCTTGGACACATATTTTAAAGCTGGA	672
Db	429	TCCAAATTTGCACCTACATTTGAAATTTGGACATCATCTTGGACACATATTTTAAAGCTGGA	488
QY	673	GAACTCACATTTTGAACCGCCGTGGGAAGAGTCCATATGACCCCTAAGCTGTGACAGC	732
Db	489	GAACTCACATTTTGAACCGCCGTGGGAAGAGTCCATATGACCCCTAAGCTGTGACAGC	548
QY	733	ATCCCTTTTAAATAGATGAGAAATTTACTCTGGAACTGCAGCTGAATTTTATGGGGCAGA	792
Db	549	ATCCCTTTTAAATAGATGAGAAATTTACTCTGGAACTGCAGCTGAATTTTATGGGGCAGA	608
QY	793	CTTTGCTATCTTCCGAACCTCTTGGGCACCAACCCCAATCAGGACAGACAGATGATTC	852
Db	609	CTTTGCTATCTTCCGAACCTCTTGGGCACCAACCCCAATCAGGACAGACAGATGATTC	668
QY	853	CAGTGGCTCAATGATCAAAAGTTCAATTAGTGCCCACTCTCATCTCAGAGAGTGACAAATCC	912
Db	669	CAGTGGCTCAATGATCAAAAGTTCAATTAGTGCCCACTCTCATCTCAGAGAGTGACAAATCC	728
QY	913	TGAAGATGACAAAGTATATCTTTTCTCCGTGAAATGCAATAGATGAGAAACACTCTGG	972
Db	729	TGAAGATGACAAAGTATATCTTTTCTCCGTGAAATGCAATAGATGAGAAACACTCTGG	788
QY	973	AAAAAGTACTCACCTAGATAGGTGAGATATGCAAGATGACATTTGGAGGGCACAGAAG	1032
Db	789	AAAAAGTACTCACCTAGATAGGTGAGATATGCAAGATGACATTTGGAGGGCACAGAAG	848
QY	1033	TCTGGTGAATAAATGGACACATCTTCTCAAGCTCGTCTGATTTGCTCAGTGCCAGGTCC	1092
Db	849	TCTGGTGAATAAATGGACACATCTTCTCAAGCTCGTCTGATTTGCTCAGTGCCAGGTCC	908
QY	1093	AAATGGCATTTGACACTCATTTTGTGAACTGCAGGATGATTCCTAATGAATTTTAAAGA	1152
Db	909	AAATGGCATTTGACACTCATTTTGTGAACTGCAGGATGATTCCTAATGAATTTTAAAGA	968
QY	1153	TCCTAAATAATCCAGTTGTATAGAGTGTGTTAAGACTTCCAGTAAACATTTTCAAGGGATC	1212
Db	969	TCCTAAATAATCCAGTTGTATAGAGTGTGTTAAGACTTCCAGTAAACATTTTCAAGGGATC	1028
QY	1213	AGCCGTGTATGTATAGCATGATGTGAGAAAGGTGTCTCTTGGTCCATATGCCCA	1272
Db	1029	AGCCGTGTATGTATAGCATGATGTGAGAAAGGTGTCTCTTGGTCCATATGCCCA	1088
QY	1273	CAGGGATGGACCCCACTATCAATCGGTGCCCTTATCAAGGAAGAGTCCCTTATCCACGGCC	1332
Db	1089	CAGGGATGGACCCCACTATCAATCGGTGCCCTTATCAAGGAAGAGTCCCTTATCCACGGCC	1148
QY	1333	AGGAACCTTGTCCAGCAACATTTGGTGGTTTGTACTCTACAAAGACCTTCTCTGATGA	1392
Db	1149	AGGAACCTTGTCCAGCAACATTTGGTGGTTTGTACTCTACAAAGACCTTCTCTGATGA	1208
QY	1393	TGTTTATAACCTTTGCAAGAGTCTATCCAGGCATGTACAATCCAGTGTTCCTATGAACA	1452
Db	1209	TGTTTATAACCTTTGCAAGAGTCTATCCAGGCATGTACAATCCAGTGTTCCTATGAACA	1268
QY	1453	TCGCCCCATAGTATCAAAACCGATGTAAATTTATCAATTTTACAAATTTGCTGTAGACCG	1512
Db	1269	TCGCCCCATAGTATCAAAACCGATGTAAATTTATCAATTTTACAAATTTGCTGTAGACCG	1328

QY	1513	AGTGGATGCAGAAGATGGACAGTATGATGTTATGTTTATCGGAAACAGATGTTGGACCGCT	1572
Db	1329	AGTGGATGCAGAAGATGGACAGTATGATGTTATGTTTATCGGAAACAGATGTTGGACCGCT	1388
QY	1573	TCTTAAAGTAGTTCCTAAATCCCTAAAGGAGACTTGGTATGATTTAGAAAGAGTTCCTGCTGA	1632
Db	1389	TCTTAAAGTAGTTCCTAAATCCCTAAAGGAGACTTGGTATGATTTAGAAAGAGTTCCTGCTGA	1448
QY	1633	AGAAATGAACAGTTCCTGGGAAACCGACTGCTATTTTCAAGCAATGGAGCTTTTCCACTAAGCA	1692
Db	1449	AGAAATGAACAGTTCCTGGGAAACCGACTGCTATTTTCAAGCAATGGAGCTTTTCCACTAAGCA	1508
QY	1693	GAAACAACTATATATTGGTTCAACGGCTGGGGTTCGCCAGCTCCCTTTTACACCGGTGCA	1752
Db	1509	GAAACAACTATATATTGGTTCAACGGCTGGGGTTCGCCAGCTCCCTTTTACACCGGTGCA	1568
QY	1753	TATTTACGGGAAAGCGTGTGCTGAGTTCCTCCGCCGAGACCTTACTGTGCTTTGGGA	1812
Db	1569	TATTTACGGGAAAGCGTGTGCTGAGTTCCTCCGCCGAGACCTTACTGTGCTTTGGGA	1628
QY	1813	TGGTTCTGCATGTTCTCGCTATTTTCCCACTGCAAGAGACCGCAAGACGACAAGATAT	1872
Db	1629	TGGTTCTGCATGTTCTCGCTATTTTCCCACTGCAAGAGACCGCAAGACGACAAGATAT	1688
QY	1873	AAGAAATGAGAGACCCCACTGACTGACTGTTTCCAGACTTACACCATGATATACCATGGCCA	1932
Db	1689	AAGAAATGAGAGACCCCACTGACTGACTGTTTCCAGACTTACACCATGATATACCATGGCCA	1748
QY	1933	CAGCCCTGAAGAGAGATCATCTATGTTGTAGAGAAATAGTAGACATTTTGGAAATGCGAG	1992
Db	1749	CAGCCCTGAAGAGAGATCATCTATGTTGTAGAGAAATAGTAGACATTTTGGAAATGCGAG	1808
QY	1993	TCGGAAGTCGAGAGAGCGCTGCTTATTGGCAATTTCCAGAGCGGCAAAATGAAGAGCGAAA	2052
Db	1809	TCGGAAGTCGAGAGAGCGCTGCTTATTGGCAATTTCCAGAGCGGCAAAATGAAGAGCGAAA	1868
QY	2053	AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCCCTTCTCCTACGTAG	2112
Db	1869	AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCCCTTCTCCTACGTAG	1928
QY	2113	TCTACAACAGAGAGGATTCAGGCAATTTACTCTGCCATCGGTGGACATGGGTTTCATACA	2172
Db	1929	TCTACAACAGAGAGGATTCAGGCAATTTACTCTGCCATCGGTGGACATGGGTTTCATACA	1988
QY	2173	AACTCTTCTTAAAGGTAAACCTCGAAAGTCATTGACACAGAGCATTTGGAAAGCACTTCTTCA	2232
Db	1989	AACTCTTCTTAAAGGTAAACCTCGAAAGTCATTGACACAGAGCATTTGGAAAGCACTTCTTCA	2048
QY	2233	TAAAGATGATGATGGAGATGGCTCTAAGACCAAGAAATGTCCAAATGACATGACACCTAG	2292
Db	2049	TAAAGATGATGATGGAGATGGCTCTAAGACCAAGAAATGTCCAAATGACATGACACCTAG	2108
QY	2293	CCAGAAGGTCTGGTACAGAGACTTTCATGACGCTCATCAACCAACCCCAATCTCAACACGAT	2352
Db	2109	CCAGAAGGTCTGGTACAGAGACTTTCATGACGCTCATCAACCAACCCCAATCTCAACACGAT	2168
QY	2353	GGATGAGTTCCTGTAAACAAAGTTTGGAAAGGAGCCGAAAAACAAAGTCCGGAAAAAGCCAGG	2412
Db	2169	GGATGAGTTCCTGTAAACAAAGTTTGGAAAGGAGCCGAAAAACAAAGTCCGGAAAAAGCCAGG	2228
QY	2413	ACATACCCCAAGGACGCTTACAAATGGAACACTTACAAAGAAATAGAAAGGTAGAAA	2472
Db	2229	ACATACCCCAAGGACGCTTACAAATGGAACACTTACAAAGAAATAGAAAGGTAGAAA	2288
QY	2473	CAGGAGGACCCCAAGAAATTTGAGAGGGCACCCAGGAGTGTCTGAGCTGATACCTCTAGA	2532
Db	2289	CAGGAGGACCCCAAGAAATTTGAGAGGGCACCCAGGAGTGTCTGAGCTGATACCTCTAGA	2348
QY	2533	AACTCTCAACAGATGAGAACTTGCCTAGACAAATTAAGTGGAAAAACAAATGCAATATACAT	2592
Db	2349	AACTCTCAACAGATGAGAACTTGCCTAGACAAATTAAGTGGAAAAACAAATGCAATATACAT	2408
QY	2593	GAACTTTTTCATGTCATTTATGTGGATGTTTACAAATGGTGGGAAATTCAGCTGAGTTCCA	2652

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Db 2409 GAACTTTTTCATGGCAATATGTCGATGTTTACAAATGGTGGAAATTCAGTCGATTTCCA 2468
Qy 2653 CCAATTATAAATAAATCATCAGTAACCTTTCCCTAATAGGCTTTT 2700
Db 2469 CCAATTATAAATAAATCAAGTAACCTTTCCCTAATAGGCTTTT 2516

RESULT 4
US-10-262-538-9
; Sequence 9, Application US/10262538
; Publication No. US20030113324A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: NEUROFILIN/VEGF-C/VEGFR-3 MATERIALS AND METHODS
; FILE REFERENCE: 28967/37564
; CURRENT APPLICATION NUMBER: US/10/262,538
; CURRENT FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 2530
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (16)..(2331)
US-10-262-538-9

Query Match 92.6%; Score 2508; DB 15; Length 2530;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 CTGAGCATGGCTGGTAACTAGGATGTCCTTTCTGGGGAGTATTACTTACAGC 252
Db 9 CTGAGCATGGCTGGTAACTAGGATGTCCTTTCTGGGGAGTATTACTTACAGC 68

Qy 253 AAGACCAATCATCAGATGGAGAGCAATGTCGCAAGCTCAATATCCTACAAAGA 312
Db 69 AAGACCAATCATCAGATGGAGAGCAATGTCGCAAGCTCAATATCCTACAAAGA 128

Qy 313 AATGTGAATCCAAATGTGATCCTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 372
Db 129 AATGTGAATCCAAATGTGATCCTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCA 188

Qy 373 TACCTTCCTTTTGGATGAGGACCGAGTAGCTGTATGTTGGAGCAAGATCACATAT 432
Db 189 TACCTTCCTTTTGGATGAGGACCGAGTAGCTGTATGTTGGAGCAAGATCACATAT 248

Qy 433 TTCAATTCACCTGGTTAATATCAAGGATTTTCAAGGATTTGTGGCCAGTATCTTACAC 492
Db 249 TTCAATTCACCTGGTTAATATCAAGGATTTTCAAGGATTTGTGGCCAGTATCTTACAC 308

Qy 493 CAGAGAGCATCAATCCAGTGGCTGGAGAGCATCTCTCAAGAGATGCTCAATTTTCA 552
Db 309 CAGAGAGCATCAATCCAGTGGCTGGAGAGCATCTCTCAAGAGATGCTCAATTTTCA 368

Qy 553 CAAGTACTTAAGGCATATATACAGACTCTTGTACGCTGTGGAAACGGGGCTTTTCA 612
Db 369 CAAGTACTTAAGGCATATATACAGACTCTTGTACGCTGTGGAAACGGGGCTTTTCA 428

Qy 613 TCCAAATTTGACCTACATTTGAATTTGACATCATCTCGAGGACAAATTTTAAAGCTGA 672
Db 429 TCCAAATTTGACCTACATTTGAATTTGACATCATCTCGAGGACAAATTTTAAAGCTGA 488

Qy 673 GAATCAATTTTGAACCGCCCTGGGAGAGTCCAATATGACCCCTAAGCTGTGACAGC 732
Db 489 GAATCAATTTTGAACCGCCCTGGGAGAGTCCAATATGACCCCTAAGCTGTGACAGC 548

Qy 733 ATCCCTTTTATAGATGAGAAATATATCTCTGGAATCTGCAAGCTGATTTTATGGGGGAGA 792
Db 549 ATCCCTTTTATAGATGAGAAATATATCTCTGGAATCTGCAAGCTGATTTTATGGGGGAGA 608

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Qy 793 CTTTGTACTTCTCCGAACTCTTTGGGCACCAACCAATCAGGACAGACAGCATGATTC 852
Db 609 CTTTGTACTTCTCCGAACTCTTTGGGCACCAACCAATCAGGACAGACAGCATGATTC 668

Qy 853 CAGGTGGCTCAATGATCCAAAGTTTCATTAGTGGCCCACTCATCTCAGAGAGTGACAAATCC 912
Db 669 CAGGTGGCTCAATGATCCAAAGTTTCATTAGTGGCCCACTCATCTCAGAGAGTGACAAATCC 728

Qy 913 TGAAGATGACAAAGTATATCTTTTCTTCCGTGAAATGCAATAGATGGAGAAACATCTGG 972
Db 729 TGAAGATGACAAAGTATATCTTTTCTTCCGTGAAATGCAATAGATGGAGAAACATCTGG 788

Qy 973 AAAAGCTACTCACGCTAGATAGTGTAGTATCCAGAGTATGCTTTGGAGGGCACAGAG 1032
Db 789 AAAAGCTACTCACGCTAGATAGTGTAGTATCCAGAGTATGCTTTGGAGGGCACAGAG 848

Qy 1033 TCTGCTGAATAAATGAGCAACATTTCTCTCAAAGCTCTCTGATTTGCTCAGTCCAGGTCC 1092
Db 849 TCTGCTGAATAAATGAGCAACATTTCTCTCAAAGCTCTCTGATTTGCTCAGTCCAGGTCC 908

Qy 1093 AATGCGCATTCAGACTCATTTTCTGATGAACTGAGGATGATTCCTAATGAATTTAAAGA 1152
Db 909 AATGCGCATTCAGACTCATTTTCTGATGAACTGAGGATGATTCCTAATGAATTTAAAGA 968

Qy 1153 TCCTAAATAATCCAGTTGTATATGAGAGTGTATTCAGACTTCCAGTAACATTTTCAAGGATC 1212
Db 969 TCCTAAATAATCCAGTTGTATATGAGAGTGTATTCAGACTTCCAGTAACATTTTCAAGGATC 1028

Qy 1213 AGCCGTGTATGTATAGCATGATGTGAGAGGGTGTTCCTTGTGTCATATGCCCA 1272
Db 1029 AGCCGTGTATGTATAGCATGATGTGAGAGGGTGTTCCTTGTGTCATATGCCCA 1088

Qy 1273 CAGGATGAGCCCAACTATCAATGGGTGCTTTATCAAGGAGAGTCCCTATCCAGGCC 1332
Db 1089 CAGGATGAGCCCAACTATCAATGGGTGCTTTATCAAGGAGAGTCCCTATCCAGGCC 1148

Qy 1333 AGGAACCTTGTCCAGAGCAACATTTGCTGTTTGTGATCTCAAGAGGACCTTCCTGATGA 1392
Db 1149 AGGAACCTTGTCCAGAGCAACATTTGCTGTTTGTGATCTCAAGAGGACCTTCCTGATGA 1208

Qy 1393 TGTATTAACCTTTGCAAGAGTCAATCCAGCATGTACAAATCCAGTGTTCCTATGAACAA 1452
Db 1209 TGTATTAACCTTTGCAAGAGTCAATCCAGCATGTACAAATCCAGTGTTCCTATGAACAA 1268

Qy 1453 TCGCCCAATAGTATCAAAACCGATCTAATTTACAAATTCACAAATTCGTAGACCG 1512
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Qy 1513 AGTGATGCAAGAGATGAGCAGTATGATTTATCGGAAACAGATGTTGGAGCCGT 1572
Db 1329 AGTGATGCAAGAGATGAGCAGTATGATTTATCGGAAACAGATGTTGGAGCCGT 1388

Qy 1573 TCTTAAAGTATTTCAATTCCTAAGAGAGCTTTGATGATTTAGAGAGGTTCTGCTGA 1632
Db 1389 TCTTAAAGTATTTCAATTCCTAAGAGAGCTTTGATGATTTAGAGAGGTTCTGCTGA 1448

Qy 1633 AGAAATGACAGTTTTCGGGAAACCGACTCTATTTTTCAGCAATGGAGCTTTCCACTAAGCA 1692
Db 1449 AGAAATGACAGTTTTCGGGAAACCGACTCTATTTTTCAGCAATGGAGCTTTCCACTAAGCA 1508

Qy 1593 GCAACAATCATATATTTGTTTCAACGGCTGGGGTTCGCCAGCTCCCTTTACACCGGTGA 1752
Db 1509 GCAACAATCATATATTTGTTTCAACGGCTGGGGTTCGCCAGCTCCCTTTACACCGGTGA 1568

Qy 1753 TATTTACGGGAAAGCGTGTGCTGAGTGTTCCTCGCCGAGACCTTACTGTGCTTGGGA 1812
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Qy 1813 TGTCTTCGATGTTCTCGCTATTTTCCCACTGCAAGAGAGCACAAGACGACAGATAT 1872
Db 1629 TGTCTTCGATGTTCTCGCTATTTTCCCACTGCAAGAGAGCACAAGACGACAGATAT 1688

Qy 1873 AAGAAATGGAGAGCCCACTCACTGTTTCAGATTTACCAATGATATATCACCATGGCCA 1932

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Db 1689 AAGAAATGAGACCCACTGACTCACTGTTGAGCTTACACCATGATAATCACCATTGCGCA 1748
Qy 1933 CAGCCCTGAAGAGAGAAATCATCTATGTTGTTAGATAATAGTAGACATTTTGGTAATCGAG 1992
Db 1749 CAGCCCTGAAGAGAGAAATCATCTATGTTGTTAGATAATAGTAGACATTTTGGTAATCGAG 1808
Qy 1993 TCCGAAGTCGAGAGAGCGCTGGTCTATTGTCATTTCCAGAGGCGAAATGAAGACGGA 2052
Db 1809 TCCGAAGTCGAGAGAGCGCTGGTCTATTGTCATTTCCAGAGGCGAAATGAAGACGGA 1868
Qy 2053 AGAAGAGATCAGAGTGGATGATCATATCATCAGACAGATCAAGGCGCTTCTGCTACCTAG 2112
Db 1869 AGAAGAGATCAGAGTGGATGATCATATCATCAGACAGATCAAGGCGCTTCTGCTACCTAG 1928
Qy 2113 TCTCAACAGAGAGATTGAGCAATTTACCTCTGCGCATGCGGTGGAACATGGGTTTCATACA 2172
Db 1929 TCTCAACAGAGAGATTGAGCAATTTACCTCTGCGCATGCGGTGGAACATGGGTTTCATACA 1988
Qy 2173 AACTCTTTTAAAGTAAACCTGGAGTCAATGATGACACAGAGATTGGAAGAACTTTCTCA 2232
Db 1989 AACTCTTTTAAAGTAAACCTGGAGTCAATGATGACACAGAGATTGGAAGAACTTTCTCA 2048
Qy 2233 TAAAGATGATGATGAGATGCTCTTAAGACCAAGAAATGTCATAGCATGACACCTAG 2292
Db 2049 TAAAGATGATGATGAGATGCTCTTAAGACCAAGAAATGTCATAGCATGACACCTAG 2108
Qy 2293 CCAGAGTCTGGTACAGAGACTTCATGACGCTCATCAACACCCCAATCTCAACAGAT 2352
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Qy 2353 GGATGAGTCTGTGAACAAAGTTTGGAAAGGCGGCAAGCAACAGTGGCAAGGCCAGG 2412
Db 2169 GGATGAGTCTGTGAACAAAGTTTGGAAAGGCGGCAAGCAACAGTGGCAAGGCCAGG 2228
Qy 2413 ACATACCCAGGGAACAGTAAACAAATGGAAGCACTTACAGAAATTAAGAAAGGTAGAAA 2472
Db 2229 ACATACCCAGGGAACAGTAAACAAATGGAAGCACTTACAGAAATTAAGAAAGGTAGAAA 2288
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Db 2289 CAGAGGACCCAGCAATTTGAGAGGCGACCCAGAGTGTCTGAGCTGCATTCCTCTAGA 2348
Qy 2533 AACCTCAACAAAGTAGAACTTGTCTAGACAAATTAACCTGGAAACAAATGCAATATACAT 2592
Db 2349 AACCTCAACAAAGTAGAACTTGTCTAGACAAATTAACCTGGAAACAAATGCAATATACAT 2408
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Db 2409 GAACCTTTTTCATGCGATATGCGATGTTTCAATGCGTGGAAATTCAGCTGAGTTCCA 2468
Qy 2653 CCAATTATAAATTAATCCATGAGTAACTTTTCCTAATAGGCTTTTTT 2700
Db 2469 CCAATTATAAATTAATCCATGAGTAACTTTTCCTAATAGGCTTTTTT 2516

RESULT 5

US-10-067-632-53
; Sequence 53, Application US/10067632
; Publication No. US20030166849A1
; GENERAL INFORMATION:

APPLICANT: Goodman, Corey S.
; Kolodkin, Alex L.
; Matthes, David
; Bentley, David R.
; O'Connor, Timothy

TITLE OF INVENTION: The Semaphorin Gene Family

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:

ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA

COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/067,632
; FILING DATE: 04-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,610
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/835,268
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..2331
; SEQUENCE DESCRIPTION: SEQ ID NO: 53:
; US-10-067-632-53

Query Match 92.6%; Score 2508; DB 15; Length 2601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 193 CTGAGCATGGCTGGTTAACTAGGATGTCGTCTTTCTGGGAGTATTACTTACAGC 252
Db 9 CTGAGCATGGCTGGTTAACTAGGATGTCGTCTTTCTGGGAGTATTACTTACAGC 68
Qy 253 AAGAGAACTATCAGATGGGAAGAACATGTCGCAAGCTGAAATATCTTACAGA 312
Db 69 AAGAGAACTATCAGATGGGAAGAACATGTCGCAAGCTGAAATATCTTACAGA 128
Qy 313 AATGTTGGAATCCAACTATGTCATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCA 372
Db 129 AATGTTGGAATCCAACTATGTCATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCA 188
Qy 373 TACCTTCCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAGGATCAATATT 432
Db 189 TACCTTCCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAGGATCAATATT 248
Qy 433 TTCTATTTCGACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTCGCGCAGTATCTTACAC 492
Db 249 TTCTATTTCGACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTCGCGCAGTATCTTACAC 308
Qy 493 CAGAAGAGATGAATCAAGTGGGCTGGAAAGACATCTCTGAAAGAAATGTGCTAATTTTCA 552
Db 309 CAGAAGAGATGAATCAAGTGGGCTGGAAAGACATCTCTGAAAGAAATGTGCTAATTTTCA 368
Qy 553 CAAGGTACTTAAGGCATATATCAGACTCACTTGTACGCTGTGGAACGGGGCTTTTCA 612
Db 369 CAAGGTACTTAAGGCATATATCAGACTCACTTGTACGCTGTGGAACGGGGCTTTTCA 428
Qy 613 TCCAATTTGCACTACATTTGAAATTTGGACATCATCTCTGAGGACAAATATTTTAAAGCTGGA 672
Db 429 TCCAATTTGCACTACATTTGAAATTTGGACATCATCTCTGAGGACAAATATTTTAAAGCTGGA 488


```

; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: COMPONDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 736
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 57
; OTHER INFORMATION: n = A,T,C or G
US-10-025-380-736

Query Match 11.2%; Score 303; DB 14; Length 354;
Best Local Similarity 99.7%; Pred. No. 5e-152;
Matches 353; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2098 CCTCTGCTAGTGTCTACAAAGAGGATTGAGGAGGATTCAGGCAATTACCTCTGCATCGGTGGA 2157
DB 1 CCTCTGCTAGTGTCTACAAAGAGGATTGAGGAGGATTCAGGCAATTACCTCTGCATCGGTGGA 60
QY 2158 ACATGGGTTTACAAACTCTTTAAAGGTAACCTGGAAGTCTTACACAGAGCATTT 2217
DB 61 ACATGGGTTTACAAACTCTTTAAAGGTAACCTGGAAGTCTTACACAGAGCATTT 120
QY 2218 GGAAGAACTTCTTCAAAAGATGATGGAGATGGCTTAAAGACCAAGAAATGTCCAA 2277
DB 121 GGAAGAACTTCTTCAAAAGATGATGGAGATGGCTTAAAGACCAAGAAATGTCCAA 180
QY 2278 TAGCATGACACCTAGCCAGAGGTTCTGGTACAGAGCTTCATGAGCTCATCAACCC 2337
DB 181 TAGCATGACACCTAGCCAGAGGTTCTGGTACAGAGCTTCATGAGCTCATCAACCC 240
QY 2338 CAATCTCAACAGTGGATGGATGGTCTGTGACACAGTTTGGAAAGGACCGAAACCAACG 2397
DB 241 CAATCTCAACAGTGGATGGATGGTCTGTGACACAGTTTGGAAAGGACCGAAACCAACG 300
QY 2398 TCGGCAAGGCGCAGGACATACCCAGGGAACAGTAACAAATGGAAGCACTTACA 2451
DB 301 TCGGCAAGGCGCAGGACATACCCAGGGAACAGTAACAAATGGAAGCACTTACA 354

RESULT 8
US-09-833-263-736
; Sequence 736, Application US/09833263
; Patent No. US20020110547A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Meagher, Madeleine J.
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND
; FILE REFERENCE: 210121.471C12
; CURRENT APPLICATION NUMBER: US/09/833,263
; CURRENT FILING DATE: 2001-04-10
; NUMBER OF SEQ ID NOS: 1093
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 736
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Homo sapien
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)...(354)
; OTHER INFORMATION: n = A,T,C or G
US-09-833-263-736

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Query Match 11.2%; Score 303; DB 9; Length 354;
Best Local Similarity 99.7%; Pred. No. 5e-152;
Matches 353; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2098 CCTCTGCTAGTGTCTACAAAGAGGATTGAGGAGGATTCAGGCAATTACCTCTGCATCGGTGGA 2157
DB 1 CCTCTGCTAGTGTCTACAAAGAGGATTGAGGAGGATTCAGGCAATTACCTCTGCATCGGTGGA 60
QY 2158 ACATGGGTTTACAAACTCTTTAAAGGTAACCTGGAAGTCTTACACAGAGCATTT 2217
DB 61 ACATGGGTTTACAAACTCTTTAAAGGTAACCTGGAAGTCTTACACAGAGCATTT 120
QY 2218 GGAAGAACTTCTTCAAAAGATGATGGAGATGGCTTAAAGACCAAGAAATGTCCAA 2277
DB 121 GGAAGAACTTCTTCAAAAGATGATGGAGATGGCTTAAAGACCAAGAAATGTCCAA 180
QY 2278 TAGCATGACACCTAGCCAGAGGTTCTGGTACAGAGCTTCATGAGCTCATCAACCC 2337
DB 181 TAGCATGACACCTAGCCAGAGGTTCTGGTACAGAGCTTCATGAGCTCATCAACCC 240
QY 2338 CAATCTCAACAGTGGATGGATGGTCTGTGACACAGTTTGGAAAGGACCGAAACCAACG 2397
DB 241 CAATCTCAACAGTGGATGGATGGTCTGTGACACAGTTTGGAAAGGACCGAAACCAACG 300
QY 2398 TCGGCAAGGCGCAGGACATACCCAGGGAACAGTAACAAATGGAAGCACTTACA 2451
DB 301 TCGGCAAGGCGCAGGACATACCCAGGGAACAGTAACAAATGGAAGCACTTACA 354

RESULT 9
US-10-025-380-736
; Sequence 736, Application US/10025380
; Publication No. US20020182191A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather

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; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: COMPONDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C14
; CURRENT APPLICATION NUMBER: US/10/025,380
; CURRENT FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 1129
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 736
; LENGTH: 354
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: 57
; OTHER INFORMATION: n = A,T,C or G
US-10-025-380-736

Query Match 11.2%; Score 303; DB 14; Length 354;
Best Local Similarity 99.7%; Pred. No. 5e-152;
Matches 353; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 2098 CCTCTGCTAGTGTCTACAAAGAGGATTGAGGAGGATTCAGGCAATTACCTCTGCATCGGTGGA 2157
DB 1 CCTCTGCTAGTGTCTACAAAGAGGATTGAGGAGGATTCAGGCAATTACCTCTGCATCGGTGGA 60
QY 2158 ACATGGGTTTACAAACTCTTTAAAGGTAACCTGGAAGTCTTACACAGAGCATTT 2217
DB 61 ACATGGGTTTACAAACTCTTTAAAGGTAACCTGGAAGTCTTACACAGAGCATTT 120
QY 2218 GGAAGAACTTCTTCAAAAGATGATGGAGATGGCTTAAAGACCAAGAAATGTCCAA 2277
DB 121 GGAAGAACTTCTTCAAAAGATGATGGAGATGGCTTAAAGACCAAGAAATGTCCAA 180
QY 2278 TAGCATGACACCTAGCCAGAGGTTCTGGTACAGAGCTTCATGAGCTCATCAACCC 2337
DB 181 TAGCATGACACCTAGCCAGAGGTTCTGGTACAGAGCTTCATGAGCTCATCAACCC 240
QY 2338 CAATCTCAACAGTGGATGGATGGTCTGTGACACAGTTTGGAAAGGACCGAAACCAACG 2397
DB 241 CAATCTCAACAGTGGATGGATGGTCTGTGACACAGTTTGGAAAGGACCGAAACCAACG 300
QY 2398 TCGGCAAGGCGCAGGACATACCCAGGGAACAGTAACAAATGGAAGCACTTACA 2451
DB 301 TCGGCAAGGCGCAGGACATACCCAGGGAACAGTAACAAATGGAAGCACTTACA 354

RESULT 10
US-09-864-761-14444
; Sequence 14444, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23

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;; PRIOR APPLICATION NUMBER: US 60/180,312
;; PRIOR FILING DATE: 2000-02-04
;; PRIOR APPLICATION NUMBER: US 60/207,456
;; PRIOR FILING DATE: 2000-05-26
;; PRIOR APPLICATION NUMBER: US 09/632,366
;; PRIOR FILING DATE: 2000-08-03
;; PRIOR APPLICATION NUMBER: GB 24263.6
;; PRIOR FILING DATE: 2000-10-04
;; PRIOR APPLICATION NUMBER: US 60/236,359
;; PRIOR FILING DATE: 2000-09-27
;; PRIOR APPLICATION NUMBER: PCT/US01/00666
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00667
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00664
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00669
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00665
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00668
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00663
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00662
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00661
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: PCT/US01/00670
;; PRIOR FILING DATE: 2001-01-30
;; PRIOR APPLICATION NUMBER: US 60/234,687
;; PRIOR FILING DATE: 2000-09-21
;; PRIOR APPLICATION NUMBER: US 09/608,408
;; PRIOR FILING DATE: 2000-06-30
;; PRIOR APPLICATION NUMBER: US 09/774,203
;; PRIOR FILING DATE: 2001-01-29
;; NUMBER OF SEQ ID NOS: 49117
;; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
;; SEQ ID NO 1444
;; LENGTH: 496
;; TYPE: DNA
;; ORGANISM: Homo sapiens
;; FEATURE:
;; OTHER INFORMATION: MAP TO AC006322.2
;; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.73
;; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.55
US-09-864-761-14444

Query Match 10.8%; Score 292; DB 9; Length 496;
Best Local Similarity 100.0%; Pred. No. 4.4e-146;
Matches 292; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 2058 AGATCAGAGTGATGATCATATCATCAGGACAGATCAAGCCCTTCTGCTACGTAGTCTAC 2117
DB 160 AGATCAGAGTGATGATCATATCATCAGGACAGATCAAGCCCTTCTGCTACGTAGTCTAC 219
QY 2118 AACAGAGGATTCAGGAATTAACCTTCCATCGCGGTGGAACATGGGTTTCATACAACTC 2177
DB 220 AACAGAGGATTCAGGAATTAACCTTCCATCGCGGTGGAACATGGGTTTCATACAACTC 279
QY 2178 TTCTTAAGGTAACCTTGGAGTCAATTCACACAGAGCAATTTGGAAGACTTCTTCATAAAG 2237
DB 280 TTCTTAAGGTAACCTTGGAGTCAATTCACACAGAGCAATTTGGAAGACTTCTTCATAAAG 339
QY 2238 ATGATGATGGAGATGGCTTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCCAGA 2297
DB 340 ATGATGATGGAGATGGCTTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCCAGA 399
QY 2298 AGGTCTGTACAGAGATTCATGACGCTCATCAACACCCCAATCTCAACAC 2349
DB 400 AGGTCTGTACAGAGATTCATGACGCTCATCAACACCCCAATCTCAACAC 451

RESULT 11
US-10-029-386-18184/c
; Sequence 18184, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEWICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 18184
; LENGTH: 164
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR7.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.59
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.4
; OTHER INFORMATION: SWISSPROT HIT: Q14563, EVALUE 4.00e-29
; OTHER INFORMATION: EST HUMAN HIT: BF667677.1, EVALUE 9.00e-81
; OTHER INFORMATION: NT HIT: gi16162409, EVALUE 1.00e-85
US-10-029-386-18184

Query Match 5.9%; Score 161; DB 15; Length 164;
Best Local Similarity 100.0%; Pred. No. 1.9e-75;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1691 CAGCAACAACACTATATTTGGTTCAACGGTGGGTTGCCAGCTCCCTTTACACGGTGT 1750
DB 164 CAGCAACAACACTATATTTGGTTCAACGGTGGGTTGCCAGCTCCCTTTACACGGTGT 105
QY 1751 GATATTTACGGGAAAGCGTGTCTGAGTGTTCCTTCGCCGAGACCCCTTACTGTGCTTGG 1810
DB 104 GATATTTACGGGAAAGCGTGTCTGAGTGTTCCTTCGCCGAGACCCCTTACTGTGCTTGG 45
QY 1811 GATGTTCTGCAATGTTCTCGCTATTTTCCCACTGCAAGAG 1851
DB 44 GATGTTCTGCAATGTTCTCGCTATTTTCCCACTGCAAGAG 4

RESULT 12
US-10-029-386-4484/c
; Sequence 4484, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: AEWICA-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 4484
; LENGTH: 591
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR7.1
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.9
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.59
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 2.4
; OTHER INFORMATION: NT HIT: gi16162409, EVALUE 4.00e-85

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; OTHER INFORMATION: SWISSPROT HIT: Q14563, EVALUE 2.00e-28
; OTHER INFORMATION: EST_HUMAN HIT: BF667677.1, EVALUE 4.00e-80
US-10-029-386-4484

Query Match      5.9%; Score 161; DB 15; Length 591;
Best Local Similarity 100.0%; Pred. No. 2.1e-75; Indels 0; Gaps 0;
Matches 161; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1691 CAGCAACAACATATATATGTTCAACGGCTGGGGTTCAGCTCCCTTTACCGGTGT 1750
Db      |||||
QY 311 CAGCAACAACATATATATGTTCAACGGCTGGGGTTCAGCTCCCTTTACCGGTGT 252
Db      |||||
QY 1751 GATATTACGGGAAGCGTGTGCTGAGTGTGCTCGCCGAGACCTTACTGTGCTGG 1810
Db      |||||
QY 251 GATATTACGGGAAGCGTGTGCTGAGTGTGCTCGCCGAGACCTTACTGTGCTGG 192
Db      |||||
QY 1811 GATGGTTCCTCATGTTCTCTGCTATTTTCCCACTGCAAGAG 1851
Db      |||||
QY 191 GATGGTTCCTCATGTTCTCTGCTATTTTCCCACTGCAAGAG 151
Db      |||||

RESULT 13
US-09-864-761-27943/c
; Sequence 27943, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1

; SEQ ID NO 27943
; LENGTH: 172
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004848.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
; OTHER INFORMATION: NT HIT: G111421514, EVALUE 8.00e-89
; OTHER INFORMATION: EST_HUMAN HIT: BF694785.1, EVALUE 2.30e+00
; OTHER INFORMATION: SWISSPROT HIT: Q14563, EVALUE 5.00e-25
US-09-864-761-27943

Query Match      5.9%; Score 160; DB 9; Length 172;
Best Local Similarity 100.0%; Pred. No. 6.7e-75; Indels 0; Gaps 0;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 310 AGAAATGTTGGAATCCAAATGTGATCACTTTCAATGGCTTGCCCAACAGCTCCAGTTA 369
Db      |||||
QY 160 AGAAATGTTGGAATCCAAATGTGATCACTTTCAATGGCTTGCCCAACAGCTCCAGTTA 101
Db      |||||
QY 370 TCATACCTTCCTTTTGGATGAGGAACGGAGTAGCTCTATGTTGGAGCAAGGATCACAT 429
Db      |||||
QY 100 TCATACCTTCCTTTTGGATGAGGAACGGAGTAGCTCTATGTTGGAGCAAGGATCACAT 41
Db      |||||
QY 430 ATTTTCATTCCAGCTGGTTAATATCAAGGATTTTCAAAG 469
Db      |||||
QY 40 ATTTTCATTCCAGCTGGTTAATATCAAGGATTTTCAAAG 1

RESULT 14
US-10-029-386-16491
; Sequence 16491, Application US/10029386
; Publication No. US20030194704A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR G
; FILE REFERENCE: Aecomica-X-2
; CURRENT APPLICATION NUMBER: US/10/029,386
; CURRENT FILING DATE: 2001-12-20
; NUMBER OF SEQ ID NOS: 34288
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 16491
; LENGTH: 191
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO CHR7.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.5
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.68
; OTHER INFORMATION: EXPRESSED IN PETAL LIVER, SIGNAL = 0.64
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.69
; OTHER INFORMATION: SWISSPROT HIT: Q14563, EVALUE 3.00e-25
; OTHER INFORMATION: NT HIT: G15174672, EVALUE 5.00e-85
US-10-029-386-16491

Query Match      5.9%; Score 160; DB 15; Length 191;
Best Local Similarity 100.0%; Pred. No. 6.7e-75; Indels 0; Gaps 0;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 310 AGAAATGTTGGAATCCAAATGTGATCACTTTCAATGGCTTGCCCAACAGCTCCAGTTA 369
Db      |||||
QY 11 AGAAATGTTGGAATCCAAATGTGATCACTTTCAATGGCTTGCCCAACAGCTCCAGTTA 70
Db      |||||
QY 370 TCATACCTTCCTTTTGGATGAGGAACGGAGTAGCTCTATGTTGGAGCAAGGATCACAT 429
Db      |||||
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Db 71 TCATACCTTCCTTTTGGATGAGAACGAGTAGCTGTATGTTGGAGCAAAAGGATCACAT 130
QY 430 ATTTTCATTCGACCTGGTTAATATCAAGGATTTTCAAAAAG 469
Db 131 ATTTTCATTCGACCTGGTTAATATCAAGGATTTTCAAAAAG 170

RESULT 15
US-09-864-761-11363/c
; Sequence 11363, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Acomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
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; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Rnmax Sequence Listing Engine vers. 1.1
; SEQ ID NO 11363
; LENGTH: 484
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC004848.1
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.3
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.1
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.2
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.2
US-09-864-761-11363

Query Match 5.9%; Score 160; DB 9; Length 484;
Best Local Similarity 100.0%; Pred. No. 7.3e-75;
Matches 160; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 310 AGAAATGTTGGAATCCAAATGTGATCACTTTCAATGCTTGGCCAAACAGCTCCAGTTA 369
Db 458 AGAAATGTTGGAATCCAAATGTGATCACTTTCAATGCTTGGCCAAACAGCTCCAGTTA 399
QY 370 TCATACCTTCCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAAAGGATCACAT 429
Db 398 TCATACCTTCCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAAAGGATCACAT 339
QY 430 ATTTTCATTCGACCTGGTTAATATCAAGGATTTTCAAAAAG 469
Db 338 ATTTTCATTCGACCTGGTTAATATCAAGGATTTTCAAAAAG 299

Search completed: September 23, 2004, 08:32:07
Job time : 2147 secs

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OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 01:33:05 ; Search time 194 Seconds
(without alignments)
7749.288 Million cell updates/sec

Title: US-09-774-490-1

Perfect score: 2709

Sequence: 1 aatcttttatttcgatg.....aggcttttttttccataacc 2709

Scoring table: OLIGO_NUC

Gapop 60.0 , Gapext 60.0

Searched: 682709 seqs, 277475446 residues

Word size : 0

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database : Issued_Patents_NA.*
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5: /cgn2_6/ptodata/2/ina/6C_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2508	92.6	2601	1	US-08-121-713D-53
2	2508	92.6	2601	1	US-08-835-268-53
3	2508	92.6	2601	2	US-09-060-622-53
4	2508	92.6	2601	3	US-08-833-391-53
5	2508	92.6	2601	4	US-09-060-610-53
6	2508	92.6	2601	5	PCT-US94-10151A-53
7	1253	46.3	1481	1	US-08-136-922-1
C 8	31	1.1	7160	4	US-08-786-531B-5
C 9	31	1.1	7235	4	US-08-786-531B-6
C 10	22	0.8	7311	4	US-09-685-004-3
C 11	22	0.8	7352	4	US-08-786-531B-4
C 12	22	0.8	7353	4	US-08-786-531B-1
C 13	22	0.8	7885	4	US-09-645-004-4
14	21	0.8	1062	4	US-09-391-741A-23
15	21	0.8	1062	4	US-09-391-741A-33
16	21	0.8	1181	4	US-09-620-312D-33
17	21	0.8	1385	3	US-08-984-288-1
18	21	0.8	1572	4	US-09-620-312D-664
19	21	0.8	1661	2	US-08-815-176-2
20	21	0.8	1661	4	US-09-187-344-2
21	21	0.8	2026	4	US-09-324-455-1
22	21	0.8	2026	4	US-09-324-455-1
C 23	20	0.7	30	3	US-08-850-961-31
C 24	20	0.7	30	3	US-09-132-541-5
C 25	20	0.7	30	4	US-09-479-776-31
26	20	0.7	840	4	US-09-244-111-5
27	20	0.7	1008	4	US-09-780-641-1
28	20	0.7	1030	4	US-09-833-381-1211
29	20	0.7	1030	4	US-09-833-381-1211

28 20 0.7 1059 4 US-09-391-741A-9 Sequence 9, Appli
29 20 0.7 1168 4 US-09-620-312D-562 Sequence 562, App
30 20 0.7 1279 3 US-08-985-950-5 Sequence 5, Appli
31 20 0.7 1279 4 US-09-546-049-5 Sequence 5, Appli
32 20 0.7 1338 4 US-09-336-536-1 Sequence 1, Appli
33 20 0.7 1503 3 US-08-999-774A-11 Sequence 11, Appli
34 20 0.7 1770 4 US-09-148-545-102 Sequence 102, App
35 20 0.7 1772 4 US-09-482-273-96 Sequence 96, Appli
36 20 0.7 1772 4 US-09-148-545-46 Sequence 46, Appli
37 20 0.7 1920 4 US-09-620-312D-7 Sequence 7, Appli
38 20 0.7 2214 4 US-09-489-847-113 Sequence 113, App
39 20 0.7 2225 4 US-09-620-312D-1046 Sequence 1046, Ap
40 20 0.7 2227 4 US-09-489-847-30 Sequence 30, Appli
41 20 0.7 2287 4 US-09-561-763-7 Sequence 7, Appli
42 20 0.7 2287 4 US-09-431-367B-7 Sequence 7, Appli
43 20 0.7 4137 3 US-09-221-235-1 Sequence 1, Appli
44 20 0.7 4137 3 US-09-221-928-1 Sequence 1, Appli
45 20 0.7 4137 3 US-09-221-527-1 Sequence 1, Appli

ALIGNMENTS

RESULT 1
US-08-121-713D-53
; Sequence 53, Application US/08121713D
; Patent No. 5639856
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713D
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..2331
; US-08-121-713D-53

Query Match 92.6%; Score 2508; DB 1; Length 2601;
Best Local Similarity 100.0%; Pred. No. 0;

Matches 2508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;			
QY	193	CTGACGATGGGCTGGTAACTAGGATGCTGCTCTTTCTGGGAGTATTAATCTTACAGC	252
Db	9	CTGACGATGGGCTGGTAACTAGGATGCTGCTCTTTCTGGGAGTATTAATCTTACAGC	68
QY	253	AAGAGCAAACTATCAGATGGGAGGAGCAATGTGCGCAAGGCTGAAATATCTTACAAGA	312
Db	69	AAGAGCAAACTATCAGATGGGAGGAGCAATGTGCGCAAGGCTGAAATATCTTACAAGA	128
QY	313	AATGTTGGAATCAACAATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCA	372
Db	129	AATGTTGGAATCAACAATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCA	188
QY	373	TACCTTCCCTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAGGATCAATATT	432
Db	189	TACCTTCCCTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAGGATCAATATT	248
QY	433	TTCAATTCGACCTGGTTAATATCAAGGATTTTCAAAAGATTGTGGCCAGTATCTTACAC	492
Db	249	TTCAATTCGACCTGGTTAATATCAAGGATTTTCAAAAGATTGTGGCCAGTATCTTACAC	308
QY	493	CAGAGAGATGAATCAAGTGGGCTGGGAAAGACATCTCTGAAAGATGTGCTTAATTTTCA	552
Db	309	CAGAGAGATGAATCAAGTGGGCTGGGAAAGACATCTCTGAAAGATGTGCTTAATTTTCA	368
QY	553	CAAGGTACTTAAGGCATATATCAGACTCACTGTGACGCTGTGGAAACGGGGCTTTTCA	612
Db	369	CAAGGTACTTAAGGCATATATCAGACTCACTGTGACGCTGTGGAAACGGGGCTTTTCA	428
QY	613	TCGAATTCGACCTAATGAAATTTGGACATCATCTCTGGAGCAAAATTTTAAAGCTGGA	672
Db	429	TCGAATTCGACCTAATGAAATTTGGACATCATCTCTGGAGCAAAATTTTAAAGCTGGA	488
QY	673	GAACTCACATTTTGAAGCGGCTGGGAGAGTCCATATGACCTTAAGCTGTGACAGC	732
Db	489	GAACTCACATTTTGAAGCGGCTGGGAGAGTCCATATGACCTTAAGCTGTGACAGC	548
QY	733	ATCCCTTTAATAGATGGAGAAATATATCTCTGGAACCTGACGTGATTTTGGGGGAGA	792
Db	549	ATCCCTTTAATAGATGGAGAAATATATCTCTGGAACCTGACGTGATTTTGGGGGAGA	608
QY	793	CTTTGCTATCTTCGAACTCTTGGGACACACCCCAATCAGGACAGAGCATGATTC	852
Db	609	CTTTGCTATCTTCGAACTCTTGGGACACACCCCAATCAGGACAGAGCATGATTC	668
QY	853	CAGGTGGCTCAATGATCCAAAGTTCATTTAGTGGCCACCTCATCTCAGAGATGACAATCC	912
Db	669	CAGGTGGCTCAATGATCCAAAGTTCATTTAGTGGCCACCTCATCTCAGAGATGACAATCC	728
QY	913	TGAAGATGACAAAGTATATCTTTCTCCGTTGAAATGCAATAGATGAGAACTCTGG	972
Db	729	TGAAGATGACAAAGTATATCTTTCTCCGTTGAAATGCAATAGATGAGAACTCTGG	788
QY	973	AAAAGTACTACCGTATAGATAGTGCAGATATGCAAGATGACCTTTGGAGGGCAGAG	1032
Db	789	AAAAGTACTACCGTATAGATAGTGCAGATATGCAAGATGACCTTTGGAGGGCAGAG	848
QY	1033	TCCTGTTGAATTAATGACCAACATTCCTCAAGCTCGTCTGATTTGCTCAGTGGCAGTCC	1092
Db	849	TCCTGTTGAATTAATGACCAACATTCCTCAAGCTCGTCTGATTTGCTCAGTGGCAGTCC	908
QY	1093	AAATGGCATTGACACTCATTTTGTATGAACTGCAGATGTTATCTCAATGAACTTTAAAGA	1152
Db	909	AAATGGCATTGACACTCATTTTGTATGAACTGCAGATGTTATCTCAATGAACTTTAAAGA	968
QY	1153	TCTTAAAAATCCAGTGTATATGAGTGTTTTACGACTTCAGTAACTTTTCAAGGGATC	1212
Db	969	TCTTAAAAATCCAGTGTATATGAGTGTTTTACGACTTCAGTAACTTTTCAAGGGATC	1028
QY	1213	AGCCGTGTGTATGTATGATCATGTGATGTGAGAGGGTGTCTTGGTCCATATGCCCA	1272
Db	1029	AGCCGTGTGTATGTATGATCATGTGATGTGAGAGGGTGTCTTGGTCCATATGCCCA	1088

QY	1273	CAGGATGGAACCACTATCAATGGTGGCTTATCAAGGAAGAGTCCCTTATCCAGGCG	1332
Db	1089	CAGGATGGAACCACTATCAATGGTGGCTTATCAAGGAAGAGTCCCTTATCCAGGCG	1148
QY	1333	AGGAACCTTGTCCGAGCAAAACATTTGGTGGTTTGTACTCTACAAGGACCTTCTGATCA	1392
Db	1149	AGGAACCTTGTCCGAGCAAAACATTTGGTGGTTTGTACTCTACAAGGACCTTCTGATCA	1208
QY	1393	TGTTATTAACCTTTTCCAAAGAGTCAATCCAGCCATGTACAATCCAGTGTCTTCTATGAACAA	1452
Db	1209	TGTTATTAACCTTTTCCAAAGAGTCAATCCAGCCATGTACAATCCAGTGTCTTCTATGAACAA	1268
QY	1453	TCGCCCAATAGTATCAAAACGGATGTAATTTATCAAAATTTGTCTAGACCG	1512
Db	1269	TCGCCCAATAGTATCAAAACGGATGTAATTTATCAAAATTTGTCTAGACCG	1328
QY	1513	AGTGGATGCAAGATGCAAGTATGATGTTATGTTTATCGGAACAGATGTTGGGACCGT	1572
Db	1329	AGTGGATGCAAGATGCAAGTATGATGTTATGTTTATCGGAACAGATGTTGGGACCGT	1388
QY	1573	TCCTAAGTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAGAGGTTCTGCTGA	1632
Db	1389	TCCTAAGTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAGAGGTTCTGCTGA	1448
QY	1633	AGAAATGACAGTGTTCGGAACCGACTGCTATTTTTCAGCAATGGAGCTTCCACTAAGCA	1692
Db	1449	AGAAATGACAGTGTTCGGAACCGACTGCTATTTTTCAGCAATGGAGCTTCCACTAAGCA	1508
QY	1693	GCAACACTATATATTTGGTTCAACGGCTGGGTTGCCAGCTCCCTTACACGGTGTGA	1752
Db	1509	GCAACACTATATATTTGGTTCAACGGCTGGGTTGCCAGCTCCCTTACACGGTGTGA	1568
QY	1753	TATTTACGGGAAAGCGTGTCTGAGTGTTCCTTCGCGCCGAGAGCTTACTGTCTTGGGA	1812
Db	1569	TATTTACGGGAAAGCGTGTCTGAGTGTTCCTTCGCGCCGAGAGCTTACTGTCTTGGGA	1628
QY	1813	TGTTTCTGCATGTTCTGCTATTTTCCACTGCAAAAGAGACGCAAGAGCAAGATAT	1872
Db	1629	TGTTTCTGCATGTTCTGCTATTTTCCACTGCAAAAGAGACGCAAGAGCAAGATAT	1688
QY	1873	AAGAAATGGAGACCCACTGACTCACTGTTTACACCTATGATAATCAACATGGCCA	1932
Db	1689	AAGAAATGGAGACCCACTGACTCACTGTTTACACCTATGATAATCAACATGGCCA	1748
QY	1933	CAGCCCTGAAGAGAGATCATCTATGGTGTAGAGATAGTACACATTTTGGATGCGAG	1992
Db	1749	CAGCCCTGAAGAGAGATCATCTATGGTGTAGAGATAGTACACATTTTGGATGCGAG	1808
QY	1993	TCCGAACTGCGAGAGAGCGCTGCTTATTTGGCAATTCAGAGCGGCAATGAAGAGCGAAA	2052
Db	1809	TCCGAACTGCGAGAGAGCGCTGCTTATTTGGCAATTCAGAGCGGCAATGAAGAGCGAAA	1868
QY	2053	AGAAGAGATCAGAGTGTGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTAG	2112
Db	1869	AGAAGAGATCAGAGTGTGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTAG	1928
QY	2113	TCTACAAACAGAGGATTCAGGCAATTAACCTCTGCCATGCGGTGGAAACATGGGTTCATACA	2172
Db	1929	TCTACAAACAGAGGATTCAGGCAATTAACCTCTGCCATGCGGTGGAAACATGGGTTCATACA	1988
QY	2173	AACCTTTTAAAGTAACTGAGTCAATGACAGAGCATTTGGAGAACTTCTTCA	2232
Db	1989	AACCTTTTAAAGTAACTGAGTCAATGACAGAGCATTTGGAGAACTTCTTCA	2048
QY	2233	TAAAGATGATGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAG	2292
Db	2049	TAAAGATGATGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAG	2108
QY	2293	CCAGAGGCTGTGTACAGAGACTTATGAGCTCATCAACCAACCACTCAACAGCAT	2352
Db	2109	CCAGAGGCTGTGTACAGAGACTTATGAGCTCATCAACCAACCACTCAACAGCAT	2168

QY 2353 GGATGAGTTCTGTGAACAAAGTTTGGAAAGGACCGAAAAACAACTGCGGCAAGGCCAGG 2412
Db 2169 CGATGAGTTCTGTGAACAAAGTTTGGAAAGGACCGAAAAACAACTGCGGCAAGGCCAGG 2228
QY 2413 ACATACCCAGGACAGTAAAGAAATGGAGACACTTACAGAAATAGAAAGGTAGAAA 2472
Db 2229 ACATACCCAGGACAGTAAAGAAATGGAGACACTTACAGAAATAGAAAGGTAGAAA 2288
QY 2473 CAGGAGGACCCACGAATTTGAGAGGCGACCCAGGAGTGTCTGAGCTGCATTACCTCTAGA 2532
Db 2289 CAGGAGGACCCACGAATTTGAGAGGCGACCCAGGAGTGTCTGAGCTGCATTACCTCTAGA 2348
QY 2533 AACCTCAACAAAGTAAAGTCTGCTAGACAAATATCTGGAATAAACAATGCAATATACAT 2592
Db 2349 AACCTCAACAAAGTAAAGTCTGCTAGACAAATATCTGGAATAAACAATGCAATATACAT 2408
QY 2593 GAACTTTTTTTCATGCAATATGATGTTTACAAATGGTGGAAATTCAGCTGAGTTCCA 2652
Db 2409 GAACTTTTTTTCATGCAATATGATGTTTACAAATGGTGGAAATTCAGCTGAGTTCCA 2458
QY 2653 CCAATATATAAATAAATCAATGATGTAATCTTCTTAATAGGCTTTTTT 2700
Db 2469 CCAATATATAAATAAATCAATGATGTAATCTTCTTAATAGGCTTTTTT 2516

RESULT 2

US-08-835-268-53
; Sequence 53, Application US/08835268
; Patent No. 5807826
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthews, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; City: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,268
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS

LOCATION: 16..2331

us-08-835-268-53

Query Match 92.6%; Score 2508; DB 1; Length 2601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 CTGAGCATGGGCTGGTTAACTAGGATTGTCTCTTTCTGGGGAGTATTACTTACAGC 252
Db 9 CTGAGCATGGGCTGGTTAACTAGGATTGTCTCTTTCTGGGGAGTATTACTTACAGC 68
QY 253 AAGAGCAAACTATCAGAAATGGGAAGAAACAATGCGCAAGGCTGAAATATATCTTACAAAGA 312
Db 69 AAGAGCAAACTATCAGAAATGGGAAGAAACAATGCGCAAGGCTGAAATATATCTTACAAAGA 128
QY 313 AATGTTGGAAATCAAACTATGATCACTTTCAATGCTGGCCAAACAGCTCCAGTTATCA 372
Db 129 AATGTTGGAAATCAAACTATGATCACTTTCAATGCTGGCCAAACAGCTCCAGTTATCA 188
QY 373 TACCTTCTCTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAAAGGATCACATATT 432
Db 189 TACCTTCTCTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAAAGGATCACATATT 248
QY 433 TTCATTGCGACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACAC 492
Db 249 TTCATTGCGACCTGGTTAATATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACAC 308
QY 493 CAGAAGAGATGAATGCAAGTGGGCTGGAAAGACATCTCTGAAAGAATGTCTAATTTTCAT 552
Db 309 CAGAAGAGATGAATGCAAGTGGGCTGGAAAGACATCTCTGAAAGAATGTCTAATTTTCAT 368
QY 553 CAAGGTACTTTAAGGCATATTAATCAGACTCATCTGTAGCGCTGTGGAAACGGGGGCTTTTCA 612
Db 369 CAAGGTACTTTAAGGCATATTAATCAGACTCATCTGTAGCGCTGTGGAAACGGGGGCTTTTCA 428
QY 613 TCCAAATTGCACTACATATGAAATTTGACATCATCTCTGAGGACAATATTTTAAAGCTGGA 672
Db 429 TCCAAATTGCACTACATATGAAATTTGACATCATCTCTGAGGACAATATTTTAAAGCTGGA 488
QY 673 GAACTCACATTTTGAATAACGGCGGTGGGAAGAGTCCATATGACCCCTAAGCTGTGACAGC 732
Db 489 GAACTCACATTTTGAATAACGGCGGTGGGAAGAGTCCATATGACCCCTAAGCTGTGACAGC 548
QY 733 ATCCCTTTTAATAGATGGGAATTTACTCTGGAAGTCTGAGCTGATTTTATGGGGGAGA 792
Db 549 ATCCCTTTTAATAGATGGGAATTTACTCTGGAAGTCTGAGCTGATTTTATGGGGGAGA 608
QY 793 CTTTGTCTATCTCCGAACCTTTTGGGCAACCAACCAACCAACCAACCAACCAACCAACCAAC 852
Db 609 CTTTGTCTATCTCCGAACCTTTTGGGCAACCAACCAACCAACCAACCAACCAACCAACCAAC 668
QY 853 CAGGTGCTCAATGATCCAAAGTTTCAATAGTGGCCACCTCATCTCAGAGAGTGACAATCC 912
Db 669 CAGGTGCTCAATGATCCAAAGTTTCAATAGTGGCCACCTCATCTCAGAGAGTGACAATCC 728
QY 913 TGAAGATGCAAAAGTATATCTTTTCTTCGTGAAATGCAATAGATGGAGAACACACTCTGG 972
Db 729 TGAAGATGCAAAAGTATATCTTTTCTTCGTGAAATGCAATAGATGGAGAACACACTCTGG 788
QY 973 AAAAGCTACTCAGCTAGAAATAGGTGAGATATGCAAGAATGACTTTTGGAGGGGACAGAAG 1032
Db 789 AAAAGCTACTCAGCTAGAAATAGGTGAGATATGCAAGAATGACTTTTGGAGGGGACAGAAG 848
QY 1033 TCTGGTGAATAATGACAAACATTTCTCAAGCTGTCTGATTTTGTCTCAGTGCAGGTCC 1092
Db 849 TCTGGTGAATAATGACAAACATTTCTCAAGCTGTCTGATTTTGTCTCAGTGCAGGTCC 908
QY 1093 AAATGCAATGACACTCATTTTGTGAACTGAGGATGATTTCTTAATGAATTTTAAAGA 1152
Db 909 AAATGCAATGACACTCATTTTGTGAACTGAGGATGATTTCTTAATGAATTTTAAAGA 968
QY 1153 TCCTAAATTCAGTTGATATGAGGTGTTTACGACTTCCAGTACATTTTCAAGGGATC 1212

STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 16...2331
US-09-060-692-53

Query Match 92.6%; Score 2508; DB 2; Length 2601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 CTGAGCAGTGGCTGGTTAACTAGGATTTCTCTCTTTCTGGGGAGTATTACTTACAGC 252
DB 9 CTGAGCAGTGGCTGGTTAACTAGGATTTCTCTCTTTCTGGGGAGTATTACTTACAGC 68
QY 253 AAGAGCAAACTATCAGAAATGGGAAGAACAAATGTGCCAAGGCTGAAATTTATCTCAAGA 312
DB 69 AAGAGCAAACTATCAGAAATGGGAAGAACAAATGTGCCAAGGCTGAAATTTATCTCAAGA 128
QY 313 AATGTTGGAATCCAAATATGATCACTTTCAATGGCTTGGCCAAAGCTCCAGTTATCA 372
DB 129 AATGTTGGAATCCAAATATGATCACTTTCAATGGCTTGGCCAAAGCTCCAGTTATCA 188
QY 373 TACCTTCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGCAAGAGATCACATATT 432
DB 189 TACCTTCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGCAAGAGATCACATATT 248
QY 433 TTCAATTCGACCTGGTTAAATATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACAC 492
DB 249 TTCAATTCGACCTGGTTAAATATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACAC 308
QY 493 CAGAGAGATCAATGCAAGTGGCTGGGAAGAGATCTCTGGAAGATGTGCTAATTTTCAT 552
DB 309 CAGAGAGATCAATGCAAGTGGCTGGGAAGAGATCTCTGGAAGATGTGCTAATTTTCAT 368
QY 553 CAAGGTACTTAAGGCATATATCAGACTCACTTGTAGCCCTGTGCAACGGGGCTTTTCA 612
DB 369 CAAGGTACTTAAGGCATATATCAGACTCACTTGTAGCCCTGTGGAACGGGGCTTTTCA 428
QY 613 TCCAAATTTGACCTACATGGAATTTGGAATTCATCTCTGAGGACAAATATTTTAAAGCTGGA 672
DB 429 TCCAAATTTGACCTACATGGAATTTGGAATTTGGAATTCATCTCTGAGGACAAATATTTTAAAGCTGGA 488
QY 673 GAACTCACATTTTGAAGAGCCCTGGGAAGAGTCCATATGACCTTAAGCTGTGACAGC 732
DB 489 GAACTCACATTTTGAAGAGCCCTGGGAAGAGTCCATATGACCTTAAGCTGTGACAGC 548
QY 733 ATCCCTTTTATAGATGGAATTTATCTCTGGAACCTGCAGCTGATTTTATGGGGCGAGA 792
DB 549 ATCCCTTTTATAGATGGAATTTATCTCTGGAACCTGCAGCTGATTTTATGGGGCGAGA 608
QY 793 CTTTGTCTATCTTCGGAACCTCTGGGACCCACCACCAATCAGACAGAGCATGATTC 852
DB 609 CTTTGTCTATCTTCGGAACCTCTGGGACCCACCACCAATCAGACAGAGCATGATTC 668
QY 853 CAGGTGGCTCAATGATCCAAAGTTCAATTAGTGCCCACTCATCTCAGAGAGTGACCAATCC 912
DB 669 CAGGTGGCTCAATGATCCAAAGTTCAATTAGTGCCCACTCATCTCAGAGAGTGACCAATCC 728
QY 913 TGAAGATGACAAAGTATCTTTTCTTCCTGGTGAATGCAATGATGGAACACCTCTGG 972
DB 729 TGAAGATGACAAAGTATCTTTTCTTCCTGGTGAATGCAATGATGGAACACCTCTGG 788
QY 973 AAAAGCTACTCACCTAGATAGTGTAGATATGCAAGATGATTTTGGAGGGCACAGAAG 1032
DB 789 AAAAGCTACTCACCTAGATAGTGTAGATATGCAAGATGATTTTGGAGGGCACAGAAG 848
QY 1033 TCTGGTGAATGAATGGAACAATTTCTCAAAAGCTGGTCTGATTTGCTCAGTCCAGGTCC 1092
DB 849 TCTGGTGAATGAATGGAACAATTTCTCAAAAGCTGGTCTGATTTGCTCAGTCCAGGTCC 908
QY 1093 AAATGGCATTTGACACTCATTTTATGATGAATGCAAGGATGATTTCTTAATGAACTTTTAAAGA 1152

DB 909 AAATGGCATTTGACACTCATTTTATGATGAATGCAAGGATGATTTCTTAATGAACTTTTAAAGA 968
QY 1153 TCCTAAATATCCAGTTGTATATGAGATGTTTACGACTTCCAGTAAACATTTTCAAGGATC 1212
DB 969 TCCTAAATATCCAGTTGTATATGAGATGTTTACGACTTCCAGTAAACATTTTCAAGGATC 1028
QY 1213 AGCGGTGTGTATGTATAGCATGATGTGGAAGAGGTTTCTCTTGGTCCATATGCCCA 1272
DB 1029 AGCGGTGTGTATGTATAGCATGATGTGGAAGAGGTTTCTCTTGGTCCATATGCCCA 1088
QY 1273 CAGGGATGGAACCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTATCCAGGCC 1332
DB 1089 CAGGGATGGAACCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTATCCAGGCC 1148
QY 1333 AGGAATCTGTCCAGCAAAACATTTTGGTGTGTTTGAATCTCAAAAGAGCTTCTCTGATGA 1392
DB 1149 AGGAATCTGTCCAGCAAAACATTTTGGTGTGTTTGAATCTCAAAAGAGCTTCTCTGATGA 1208
QY 1393 TGTATAAACCCTTTGCAAGAGTCCAGCCATGTACAATCCAGTGTCTTCTATGAACAA 1452
DB 1209 TGTATAAACCCTTTGCAAGAGTCCAGCCATGTACAATCCAGTGTCTTCTATGAACAA 1268
QY 1453 TCSCCCTAATAGTATCAAAACCGATGTAAATTTATCAATTTACAAATTTGTCTGACCG 1512
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QY 1513 AGTGGATGCAAGAGTGGACAGTATGATGTATGTTTATCGGAACAGATGTTGGGACCGT 1572
DB 1329 AGTGGATGCAAGAGTGGACAGTATGATGTATGTTTATCGGAACAGATGTTGGGACCGT 1388
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DB 1389 TCTTAAAGTAGTTTCAATTTCTTAAAGAGACTTGGTATGATTTTGAAGAGGTTCTGCTGA 1448
QY 1633 AGAATATGACAGTTTTCGGGAACCGACTCTATTTTTCAGCAATGGAGCTTTCCACATGA 1692
DB 1449 AGAATATGACAGTTTTCGGGAACCGACTCTATTTTTCAGCAATGGAGCTTTCCACATGA 1508
QY 1693 GCAACAACTATATATTTTCCCACTGCAAGAGAGAGCAGCAACAGCAAGATAT 1872
DB 1509 GCAACAACTATATATTTTCCCACTGCAAGAGAGAGCAGCAACAGCAAGATAT 1688
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DB 1569 TATTTTACGGGAAGCGTGTGCTGAGTGTGCTTCCCGGAGACCTTACTGTCTTGGGA 1628
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QY 1873 AAGAATGGAAGACCCACTGACTCTGCTGAGCTTACACCATGATATACCATGGCCA 1932
DB 1689 AAGAATGGAAGACCCACTGACTCTGCTGAGCTTACACCATGATATACCATGGCCA 1748
QY 1933 CAGCCCTGAAGAGAGAAATCATCTATGTTGAGAGATAGTAGCAATTTTGGATGAG 1992
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QY 1993 TCCGAAGTGCAGAGAGCGCTGGTCTATTTGGCAATTTCCAGAGGGGAAATGAAGACGAAA 2052
DB 1809 TCCGAAGTGCAGAGAGCGCTGGTCTATTTGGCAATTTCCAGAGGGGAAATGAAGACGAAA 1868
QY 2053 AGAAGAGATCAGAGTGGATGATCATATCATCAGACAGATCAAGGCTTCTGCTACGTAG 2112
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QY 2113 TCTCAACAGAGAGGATTCAGGCAATTTACTCTGCTCATCGGTGGAACATGGTTTCATACA 2172
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QY 2173 AACTCTTCTTAAAGGTAAACCTTGGAGTGTATGACAGAGCATTTTGGAGAACTTCTTCA 2232

QY 1033 TCTGTGTAATAAATGGAACAACATTCCTCAAAAGTCGTCTGATTTTCTCAGTGCAGGTCC 1092
Db 849 TCTGTGTAATAAATGGAACAACATTCCTCAAAAGTCGTCTGATTTTCTCAGTGCAGGTCC 908
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Db 909 AAATGSCATTGACACTCAATTTTGTATGAACTGCAAGATGTATTCCTAATGAATTTAAAGA 968
QY 1153 TCCTAAAAATCCAGTTGTATATGAGAGTGTATACGACTTCCAGTAAACATTTTCAAGGGATC 1212
Db 969 TCCTAAAAATCCAGTTGTATATGAGAGTGTATACGACTTCCAGTAAACATTTTCAAGGGATC 1028
QY 1213 AGCCGTGTATGTATATGAGAGTGTATACGACTTCCAGTAAACATTTTCAAGGGATC 1272
Db 1029 AGCCGTGTATGTATATGAGAGTGTATACGACTTCCAGTAAACATTTTCAAGGGATC 1088
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Db 1149 AGGAATCTGTCCAGCAAAAACATTTGGTGTATGAGTCTCTCAAGAGACCTTCTCTGATGA 1208
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Db 1629 TGGTCTGCAATGTTCTGCTATTTTCCACTGCAAGAGAGCGCAAGACGCAAGATAT 1688
QY 1873 AAGAAATGGAGACCCACTGACTCTGCTGAGTGTGCTCGCCGAGACCTTACTGTGCTGGGA 1932
Db 1689 AAGAAATGGAGACCCACTGACTCTGCTGAGTGTGCTCGCCGAGACCTTACTGTGCTGGGA 1748
QY 1933 CAGCCCTGAGAGAGATCATCTATGTTGTAGAGATAGTAGACATTTTGAATGCGAG 1992
Db 1749 CAGCCCTGAGAGAGATCATCTATGTTGTAGAGATAGTAGACATTTTGAATGCGAG 1808
QY 1993 TCCGAAGTCGAGAGAGCGTGTGTTATGCGCAATTCAGAGCGGAATGAAGAGCGAA 2052
Db 1809 TCCGAAGTCGAGAGAGCGTGTGTTATGCGCAATTCAGAGCGGAATGAAGAGCGAA 1868
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Db 1869 AGAAGATCAGAGTGGATCATATCATCAGACAGATCAAGGCTTCTGTACGTAG 1928
QY 2113 TCTACACAGAGATTCAGGCAATTACCTCTCCATCGGTGGAACATGGTTCTATACA 2172

Db 1929 TCTACACAGAGATTCAGGCAATTACCTCTCCATCGGTGGAACATGGTTCTATACA 1988
QY 2173 AACTCTTTTAAAGTAAACCTTGAAGTCAATGACAGAGCATTTGGAAGAACTTCTTCA 2232
Db 1989 AACTCTTTTAAAGTAAACCTTGAAGTCAATGACAGAGCATTTGGAAGAACTTCTTCA 2048
QY 2233 TAAAGATGATGATGAGAGTGGCTTAAGACCAAGAAATGTCCTCAATAGCATGACACCTAG 2292
Db 2049 TAAAGATGATGATGAGAGTGGCTTAAGACCAAGAAATGTCCTCAATAGCATGACACCTAG 2108
QY 2293 CAGAGAGTCTGTTAAGAGATTCATGAGTCTATCAACCCCAATCTCAACACGAT 2352
Db 2109 CAGAGAGTCTGTTAAGAGATTCATGAGTCTATCAACCCCAATCTCAACACGAT 2168
QY 2353 GAGTGTGTTCTGTAACAAAGTTTGAAGAGGACGAAACACGTCGCAAGGCGAG 2412
Db 2169 GAGTGTGTTCTGTAACAAAGTTTGAAGAGGACGAAACACGTCGCAAGGCGAG 2228
QY 2413 ACATACCCAGGAAACAGTAAACAAATGGAAGCACCTTACAGAAATTAAGAAAGGTAGAAA 2472
Db 2229 ACATACCCAGGAAACAGTAAACAAATGGAAGCACCTTACAGAAATTAAGAAAGGTAGAAA 2288
QY 2473 CAGAGAGCCAGCAATTTGAGAGGACCCAGAGTGTCTGAGTGCATTTACCTCTAGA 2532
Db 2289 CAGAGAGCCAGCAATTTGAGAGGACCCAGAGTGTCTGAGTGCATTTACCTCTAGA 2348
QY 2533 AACCTCAAAACAGTAGAAACTTGCCTAGACAACTAACTGGAAGAAACAAATGCAATATACAT 2592
Db 2349 AACCTCAAAACAGTAGAAACTTGCCTAGACAACTAACTGGAAGAAACAAATGCAATATACAT 2408
QY 2593 GAACTTTTCTATGGAATATGAGATGTTTCAATGTTGGAAGTAACTGAGTGCATTTCA 2652
Db 2409 GAACTTTTCTATGGAATATGAGATGTTTCAATGTTGGAAGTAACTGAGTGCATTTCA 2468
QY 2653 CCAATTTAAATTAATCCATCAGTAACTTCTCTAATAGGCTTTTCTT 2700
Db 2469 CCAATTTAAATTAATCCATCAGTAACTTCTCTAATAGGCTTTTCTT 2516

RESULT 5

US-09-060-610-53
; Sequence 53, Application US/09060610
; Patent No. 6344544
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060.610
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/835,268
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.

```

; REGISTRATION NUMBER: 36.627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..2331
; US-09-060-610-53

Query Match 92.6%; Score 2508; DB 4; Length 2601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 CTGACGATGGGCTGTTAACTAGGATGCTGCTGCTTTCTGGGAGTATTACTTACAGC 252
DB 9 CTGACGATGGGCTGTTAACTAGGATGCTGCTGCTTTCTGGGAGTATTACTTACAGC 68

QY 253 AAGAGCAACTATCAGATGGGAGAGCAATGTGCCAAGGCTGAATATCTTACAAGA 312
DB 69 AAGAGCAACTATCAGATGGGAGAGCAATGTGCCAAGGCTGAATATCTTACAAGA 128

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QY 433 TTCAATTCGACCTGGTAAATATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACAC 492
DB 249 TTCAATTCGACCTGGTAAATATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACAC 308

QY 493 CAGAGAGATGAATCGAAGTGGCTGGGAAAGACATCTGAAAGAAATGCTCAATTT 552
DB 309 CAGAGAGATGAATCGAAGTGGCTGGGAAAGACATCTGAAAGAAATGCTCAATTT 368

QY 553 CAAGGTACTTAAGGCATATAATCAGACTCACTTGTAGCCCTGTGGAAACGGGGCTTTTCA 612
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QY 613 TCCAAATTCACCTACATGAAATGGACATCATCTTGAGGACAAATATTTTAAAGTGA 672
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QY 673 GAACCTACATTTTGAAGACGGCTGGGAGAGATCCATATGACCCCTAAGCTGTGACAGC 732
DB 489 GAACCTACATTTTGAAGACGGCTGGGAGAGATCCATATGACCCCTAAGCTGTGACAGC 548

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DB 609 CTTTGTCTATCTTCCGAATCTTTGGGACACCAACCCCAATCAGACAGAGCATGATTC 668

QY 853 CAGGTGGCTCAATGATCCAAAGTTTCAATTTAGTGGCCCACTCATCTCAGAGATGACATCC 912
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QY 913 TGAAGATGACAAAGTATATCTTTTCTCCGTGAAAAATGCAATAGATGGAGAACACTCTGG 972
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QY 1933 CAGCCCTGAGAGAGAGATCATCTATGCTGTAGAGATAGTAGACATTTTGGATGAG 1992
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QY 1993 TCCGAAGTCCGAGAGAGCGCTGTCTATTGGCAATTCAGAGGCGGAATGAAGAGCGAAA 2052
DB 1809 TCCGAAGTCCGAGAGAGCGCTGTCTATTGGCAATTCAGAGGCGGAATGAAGAGCGAAA 1868

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QY 2053 AGAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTACGTAG 2112
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QY 2113 TCTACAAAGAGAGATTCAGGCAATTAACCTCTGCCATCGGTGGAACAATGGGTTTATACA 2172
DB 1929 TCTACAAAGAGAGATTCAGGCAATTAACCTCTGCCATCGGTGGAACAATGGGTTTATACA 1988
QY 2173 AACTCTTCTTAAGGTAACTCTGGAAGTCAATTCACACAGAGATTTGGAAGAACTTTCTCA 2232
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DB 2109 CCAGAGTCTGTTACAGAGACTTTCATCAGCTCATCAACACCCCAATCTCAACAGAT 2168
QY 2353 GGATGAGTCTGTGAACAAAGTTTGAAGAGGACCGAAGCAACAGCTGGCAAGGCCAGG 2412
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DB 2349 AACCTCAACAAAGTAGAACTTGCCTAGACAAATTAAGTGAAGAAACAAATGCAATATACAT 2408
QY 2593 GAACTTTTTCATGCAATATGAGATGTTTACAAATGTTGGAATTCAGCTGAGTTCCA 2652
DB 2409 GAACTTTTTCATGCAATATGAGATGTTTACAAATGTTGGAATTCAGCTGAGTTCCA 2468
QY 2653 CCAATTATAATTAATCCATGAGTAACTTTCTTAATAGGCTTTTTT 2700
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RESULT 6

PCT-US94-10151A-53

; Sequence 53, Application PC/TUS9410151A

; GENERAL INFORMATION:

; APPLICANT: The Regents of the University of California

; TITLE OF INVENTION: The Semaphorin Gene Family

; NUMBER OF SEQUENCES: 66

; CORRESPONDENCE ADDRESS:

; ADDRESS: FLEHR HOEBACH TEST ALBRITTON & HERBERT

; STREET: 4 Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: CA

; COUNTRY: USA

; ZIP: 94111-4187

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US94/10151A

; FILING DATE: 13-SEP-1994

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Osman, Richard A.

; REGISTRATION NUMBER: 36,627

; REFERENCE/DOCKET NUMBER: FP-58750-PC/RAO

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299 FHT UR
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; NAME/KEY: CDS
; LOCATION: 16..2331
; PCT-US94-10151A-53

Query Match 92.8%; Score 2508; DB 5; Length 2601;

Best Local Similarity 100.0%; Pred. No. 0;

Matches 2508; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 CTCGACGATGGGCTGTTAACTAGGATTCCTGCTCTTTCTGGGAGTATTACTTACAGC 252
DB 9 CTCGACGATGGGCTGTTAACTAGGATTCCTGCTCTTTCTGGGAGTATTACTTACAGC 68
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DB 69 AAGAGCAAACTATCAGATGGGAAGAAACAATGTGCAAGGCTGAAATATCTCTACAAAG 128
QY 313 AATGTTGGATCAACAATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCA 372
DB 129 AATGTTGGATCAACAATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCA 188
QY 373 TACCTTCTCTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAGGATCACATAT 432
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QY 433 TTCATTCGACCTGGTTTAATATCAAGGATTTTCAAAAGATTTGTGSCCAGTATCTTACAC 492
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DB 369 CAAGGTACTTAAGGCATATAATCAGACTCATCTGTACGCTGTGAAACGGGGCTTTTCA 428
QY 613 TCCAAATTCGACCTCATTTGAAATGGACATCATCTGAGGACATATTTTAAAGCTGA 672
DB 429 TCCAAATTCGACCTCATTTGAAATGGACATCATCTGAGGACATATTTTAAAGCTGA 488
QY 673 GAACTCACAATTTTGAAGACGGCGGTGGGAAGTCCATATGACCTTAAGCTGCTGACAGC 732
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QY 793 CTTTGTCTATCTTCCGAACTCTTTGGGCAACCAACCAATCAGGACAGAGCATGATTC 852
DB 609 CTTTGTCTATCTTCCGAACTCTTTGGGCAACCAACCAATCAGGACAGAGCATGATTC 668
QY 853 CAGGTGGCTCAATGATCCAAAGTTTCAATAGTCCCACTCTCTCAGAGAGTGACAAATCC 912
DB 669 CAGGTGGCTCAATGATCCAAAGTTTCAATAGTCCCACTCTCTCAGAGAGTGACAAATCC 728
QY 913 TGAAGATGACAAAGTATATCTTTTCTTCGTCGAAATGCAATAGATGGAGACACTCTGG 972
DB 729 TGAAGATGACAAAGTATATCTTTTCTTCGTCGAAATGCAATAGATGGAGACACTCTGG 788
QY 973 AAAAGCTACTCAGCTAGATAGGTCAGATATGCAAGATAGCTTTGGAGGSCACAGAG 1032

TELECOMMUNICATION INFORMATION:

TELEPHONE: 215-568-3100

TELEFAX: 215-568-3439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 1481 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: both

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 50..1480

US-08-136-922-1

Query Match 46.3%; Score 1253; DB 1; Length 1481;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1303; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY	904	TGCAATCCTGAAGATGACAAAGTATATCTTTTCTCCGTGAAATCAATAGATGAGA	963
DB	58	TGCAATCCTGAAGATGACAAAGTATATCTTTTCTCCGTGAAATCAATAGATGAGA	117
QY	964	ACACTCTGGAAGCTACTACCGCTAGATAGTTCAGATATGCAAGATGACTTTGAGG	1023
DB	118	ACACTCTGGAAGCTACTACCGCTAGATAGTTCAGATATGCAAGATGACTTTGAGG	177
QY	1024	GCACAGAGTCTGCTGTAATAATGGACAACTTCTCAAAGCTCGTCTGCTCAGT	1083
DB	178	GCACAGAGTCTGCTGTAATAATGGACAACTTCTCAAAGCTCGTCTGCTCAGT	237
QY	1084	GCCAGGTCCTGAATGCACTCACTTTGATGAGTCACTGAGATGATTCCTAATGAA	1143
DB	238	GCCAGGTCCTGAATGCACTCACTTTGATGAGTCACTGAGATGATTCCTAATGAA	297
QY	1144	CTTTAAAGATCCTAAATCAGTTGATATGAGAGTGTACGACTTCCAGTACATTTT	1203
DB	298	CTTTAAAGATCCTAAATCAGTTGATATGAGAGTGTACGACTTCCAGTACATTTT	357
QY	1204	CAAGGATACCGGTGTATGTATAGCATGATGATGAGAGGTTTCCTTGTTCC	1263
DB	358	CAAGGATACCGGTGTATGTATAGCATGATGATGAGAGGTTTCCTTGTTCC	417
QY	1264	ATATGCCACAGGATGACCACTATCAATGGTGGCTTATCAAGAGAGTCCCTTA	1323
DB	418	ATATGCCACAGGATGACCACTATCAATGGTGGCTTATCAAGAGAGTCCCTTA	477
QY	1324	TCCAGGCGCAGAACTTGTCCAGCAAAACATTTGGTGGTTTGACTCTACAAAGACCT	1383
DB	478	TCCAGGCGCAGAACTTGTCCAGCAAAACATTTGGTGGTTTGACTCTACAAAGACCT	537
QY	1384	TCCTGATGATGTATTAACCTTGCAGAAAGTATCCAGCCATGTACATCCAGTGTTC	1443
DB	538	TCCTGATGATGTATTAACCTTGCAGAAAGTATCCAGCCATGTACATCCAGTGTTC	597
QY	1444	TATGAACATCCCAATAGTATGATCAAAAGGATGTAATATCAATTTACACAAATGT	1503
DB	598	TATGAACATCCCAATAGTATGATCAAAAGGATGTAATATCAATTTACACAAATGT	657
QY	1504	CGTAGACCGAGTGGATGAGAGATGAGACATGATGTTATGTTATCGGAACAGATG	1563
DB	658	CGTAGACCGAGTGGATGAGAGATGAGACATGATGTTATGTTATCGGAACAGATG	717
QY	1564	TGGGACCTTCTTAAGTAGTTTCAATTCCTAAGGAGCTGGTATGATTTAGAGAGGT	1623
DB	718	TGGGACCTTCTTAAGTAGTTTCAATTCCTAAGGAGCTGGTATGATTTAGAGAGGT	777
QY	1624	TCTGCTGGAAGAAATGACAGTTTTCGGGAACCGACTCTATTTTTCAGCAATGGAGCTTC	1683
DB	778	TCTGCTGGAAGAAATGACAGTTTTCGGGAACCGACTCTATTTTTCAGCAATGGAGCTTC	837
QY	1684	CACTAAGCAGCAACCACTATATATTTGGTTCAACGGCTGGGTGCGGAGCTCCCTTTACA	1743

RESULT 8

US-08-786-531B-5/c

; Sequence 5, Application US/08786531B

; Patent No. 6541197

; GENERAL INFORMATION:

; APPLICANT: Link, Charles J.

; APPLICANT: Levy, John P.

; APPLICANT: Wang, Suming

; APPLICANT: Seragina, Tatiana

; TITLE OF INVENTION: Vehicles for Stable Transfer of Green

; TITLE OF INVENTION: Fluorescent Protein Gene and Methods of Use for Same

; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:

; ADDRESSES: Zarley, McKee, Thomte, Voorhees & Sease

; STREET: 801 Grand Suite 3200

; CITY: Des Moines

; STATE: Iowa

; COUNTRY: United States

; ZIP: 50309

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent in Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/786,531B

; FILING DATE: 21-JAN-1997

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 60/010371

; FILING DATE: 22-JAN-1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Nebel, Heidi S.

; REGISTRATION NUMBER: 37,719

; REFERENCE/DOCKET NUMBER: hgri

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 515-288-3667

; TELEFAX: 515-288-1338

DB	838	CACAAAGCAGCAACAACTATATATTTGGTTCAACGGCTGGGGTTGCCAGCTCCCTTTACA	897
QY	1744	CCGGTGTGATATTTACGGGAAAGCGTGTGCTGAGTGTTCCTCGCCCGAGACCTTACTG	1803
DB	898	CCGGTGTGATATTTACGGGAAAGCGTGTGCTGAGTGTTCCTCGCCCGAGACCTTACTG	957
QY	1804	TGCTTGGGATGTTCTTCGATGTTCTCGTATTTTCCCACTGCAAAAGACGCAAGAGG	1863
DB	958	TGCTTGGGATGTTCTTCGATGTTCTCGTATTTTCCCACTGCAAAAGACGCAAGAGG	1017
QY	1864	ACAGATATAAGAAATGGAGCCCACTGACTCCTGTTTCCAGACTTACACCATGATAATCA	1923
DB	1018	ACAAGATATAAGAAATGGAGCCCACTGACTCCTGTTTCCAGACTTACACCATGATAATCA	1077
QY	1924	CCATGGCCACAGCCCTGAAGACAGAGAAATCATCTATGTTGTAGAGAAATAGTAGCACATTTT	1983
DB	1078	CCATGGCCACAGCCCTGAAGACAGAGAAATCATCTATGTTGTAGAGAAATAGTAGCACATTTT	1137
QY	1984	GAATGTCAGTCCGAAGTCCAGAGAGCGTGTCTATTGGCAATTCAGAGCGGAAATGA	2043
DB	1138	GAATGTCAGTCCGAAGTCCAGAGAGCGTGTCTATTGGCAATTCAGAGCGGAAATGA	1197
QY	2044	AGAGCGAAAGAGAGATCAGAGTGGATCATATCATCATCAGACAGATCAAGGCTTCT	2103
DB	1198	AGAGCGAAAGAGAGATCAGAGTGGATCATATCATCATCAGACAGATCAAGGCTTCT	1257
QY	2104	GCTACGTACTCTACAAAGAGATTCAGGCAATTAACCTTCCCATGCGGTGGAACATGG	2163
DB	1258	GCTACGTACTCTACAAAGAGATTCAGGCAATTAACCTTCCCATGCGGTGGAACATGG	1317
QY	2164	GTTCTACAAACTCTTTTAAAGTAAACCTGGAAGTCAATTGACA	2207
DB	1318	GTTCTACAAACTCTTTTAAAGTAAACCTGGAAGTCAATTGACA	1361

INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 7160 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-786-531B-5

Query Match 1.1%; Score 31; DB 4; Length 7160;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATCTTTTATTTATCGATGTTAACAGCTT 31
Db 4179 AATCTTTTATTTATCGATGTTAACAGCTT 4149

RESULT 9

US-08-786-531B-6/c
Sequence 6, Application US/08786531B
Patent No. 6541197

GENERAL INFORMATION:
APPLICANT: Link, Charles J.
APPLICANT: Levy, John P.
APPLICANT: Wang, Suming
APPLICANT: Seregina, Tatiana
TITLE OF INVENTION: Vehicles for Stable Transfer of Green
TITLE OF INVENTION: Fluorescent Protein Gene and Methods of Use for Same
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zarley, McKee, Thome, Voorhees & Sease
STREET: 801 Grand Suite 3200
CITY: Des Moines
STATE: Iowa
COUNTRY: United States
ZIP: 50309

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,531B
FILING DATE: 21-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/010371
FILING DATE: 22-JAN-1996

ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: Hgttri
TELECOMMUNICATION INFORMATION:
TELEPHONE: 515-288-3667
TELEFAX: 515-288-1338
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 7235 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-786-531B-6

Query Match 1.1%; Score 31; DB 4; Length 7235;
Best Local Similarity 100.0%; Pred. No. 4.3e-05;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATCTTTTATTTATCGATGTTAACAGCTT 31
Db 4254 AATCTTTTATTTATCGATGTTAACAGCTT 4224

RESULT 10

US-09-645-004-3/c
Sequence 3, Application US/09645004
Patent No. 6608238

GENERAL INFORMATION:
APPLICANT: Gavora, Jan S.
APPLICANT: Falconer, Marcia M.
APPLICANT: Nguyen, Thuy H.
APPLICANT: Benkel, Bernhard F.
TITLE OF INVENTION: Trans-Somatics With Gene Transfer Into Mammary Epithelial Cells
FILE REFERENCE: GALA-06402
CURRENT APPLICATION NUMBER: US/09/645,004
CURRENT FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patent in version 3.2
SEQ ID NO 3
LENGTH: 7311
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Plasmid pLNMX
US-09-645-004-3

Query Match 0.8%; Score 22; DB 4; Length 7311;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AATCTTTTATTTATCGATGTT 22
Db 4330 AATCTTTTATTTATCGATGTT 4309

RESULT 11

US-08-786-531B-4/c
Sequence 4, Application US/08786531B
Patent No. 6541197

GENERAL INFORMATION:
APPLICANT: Link, Charles J.
APPLICANT: Levy, John P.
APPLICANT: Wang, Suming
APPLICANT: Seregina, Tatiana
TITLE OF INVENTION: Vehicles for Stable Transfer of Green
TITLE OF INVENTION: Fluorescent Protein Gene and Methods of Use for Same
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zarley, McKee, Thome, Voorhees & Sease
STREET: 801 Grand Suite 3200
CITY: Des Moines
STATE: Iowa
COUNTRY: United States
ZIP: 50309

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,531B
FILING DATE: 21-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/010371
FILING DATE: 22-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: Hgttri
TELECOMMUNICATION INFORMATION:

TELEPHONE: 515-288-3667
TELEFAX: 515-288-1338
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 7352 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-786-531B-4

Query Match 0.8%; Score 22; DB 4; Length 7352;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATCTTTTATTTATCGATGTT 22
|||||
DB 4371 AATCTTTTATTTATCGATGTT 4350

RESULT 12

US-08-786-531B-1/c
Sequence 1, Application US/08786531B
Patent No. 6541197

GENERAL INFORMATION:

APPLICANT: Link, Charles J.
APPLICANT: Levy, John P.
APPLICANT: Wang, Suming
APPLICANT: Serregina, Tatiana
TITLE OF INVENTION: Vehicles for Stable Transfer of Green
TITLE OF INVENTION: Fluorescent Protein Gene and Methods of Use for Same
NUMBER OF SEQUENCES: 10
CORRESPONDENCE ADDRESS:
ADDRESSEE: Zarley, McKee, Thomte, Voorhees & Sease
STREET: 801 Grand Suite 3200
CITY: Des Moines
STATE: Iowa
COUNTRY: United States
ZIP: 50309

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786.531B
FILING DATE: 21-JAN-1997

CLASSIFICATION:

435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/010371
FILING DATE: 22-JAN-1996
ATTORNEY/AGENT INFORMATION:
NAME: Nebel, Heidi S.
REGISTRATION NUMBER: 37,719
REFERENCE/DOCKET NUMBER: Rguri
TELEPHONE: 515-288-3667
TELEFAX: 515-288-1338

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 7353 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: circular
MOLECULE TYPE: other nucleic acid
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-786-531B-1

Query Match 0.8%; Score 22; DB 4; Length 7353;
Best Local Similarity 100.0%; Pred. No. 0.97;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AATCTTTTATTTATCGATGTT 22
|||||
DB 4372 AATCTTTTATTTATCGATGTT 4351

RESULT 13

US-09-645-004-4/c
Sequence 4, Application US/09645004
Patent No. 6608238

GENERAL INFORMATION:

APPLICANT: Gavora, Jan S.
APPLICANT: Falconer, Marcia M.
APPLICANT: Nguyen, Thuy H.
APPLICANT: Benkel, Bernhard F.
TITLE OF INVENTION: Trans-Somatics With Gene-Transfer Into Mammary Epithelial Cells
FILE REFERENCE: GALA-06402
CURRENT APPLICATION NUMBER: US/09/645,004
CURRENT FILING DATE: 2000-08-24
NUMBER OF SEQ ID NOS: 4
SOFTWARE: Patent in version 3.2
SEQ ID NO 4
LENGTH: 7885
TYPE: DNA
ORGANISM: Artificial
FEATURE:
OTHER INFORMATION: Plasmid pLNMi2X
US-09-645-004-4

Query Match

0.8%; Score 22; DB 4; Length 7885;
Best Local Similarity 100.0%; Pred. No. 0.97;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AATCTTTTATTTATCGATGTT 22
|||||
DB 4904 AATCTTTTATTTATCGATGTT 4883

RESULT 14

US-09-391-741A-23
Sequence 23, Application US/09391741A
Patent No. 6555732

GENERAL INFORMATION:

APPLICANT: Duvick, Jonathan P.
APPLICANT: Sharma, Yogesh Kumar
TITLE OF INVENTION: Rac-Like Genes and Methods of Use
FILE REFERENCE: 0866D
CURRENT APPLICATION NUMBER: US/09/391,741A
CURRENT FILING DATE: 1999-09-08

PRIOR APPLICATION NUMBER: 60/111,919

PRIOR FILING DATE: 1998-12-11

PRIOR APPLICATION NUMBER: 60/100,284

PRIOR FILING DATE: 1998-09-14

PRIOR APPLICATION NUMBER: 09/391,741

PRIOR FILING DATE: 1999-09-08

NUMBER OF SEQ ID NOS: 51

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 23

LENGTH: 1062

TYPE: DNA

ORGANISM: Zea mays

FEATURE:

NAME/KEY: CDS

LOCATION: (172)...(807)

US-09-391-741A-23

Query Match 0.8%; Score 21; DB 4; Length 1062;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 GTCGACCCACGGCTCCGGGAG 77
|||||

Thu Sep 23 08:54:05 2004

Db 3 GTCGACCCACGCGTCCGGGAG 23

RESULT 15

US-09-391-741A-33
 ; Sequence 33, Application US/09391741A
 ; Patent No. 6555732
 ; GENERAL INFORMATION:
 ; APPLICANT: Duwick, Jonathan P.
 ; APPLICANT: Sharma, Yogesh Kumar
 ; TITLE OF INVENTION: Rac-Like Genes and Methods of Use
 ; FILE REFERENCE: 0866D
 ; CURRENT APPLICATION NUMBER: US/09/391,741A
 ; CURRENT FILING DATE: 1999-09-08
 ; PRIOR APPLICATION NUMBER: 60/111,919
 ; PRIOR FILING DATE: 1998-12-11
 ; PRIOR APPLICATION NUMBER: 60/100,284
 ; PRIOR FILING DATE: 1998-09-14
 ; PRIOR APPLICATION NUMBER: 09/391,741
 ; PRIOR FILING DATE: 1999-09-08
 ; NUMBER OF SEQ ID NOS: 51
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 33
 ; LENGTH: 1062
 ; TYPE: DNA
 ; ORGANISM: Zea mays
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (172)...(807)
 US-09-391-741A-33

Query Match 0.8%; Score 21; DB 4; Length 1062;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 57 GTCGACCCACGCGTCCGGGAG 77
 |||||
 Db 3 GTCGACCCACGCGTCCGGGAG 23

Search completed: September 23, 2004, 05:10:25
 Job time : 204 secs

Result	Query	Score	Length	ID	Description
No.	Match		DB	ID	

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CURRENT APPLICATION NUMBER: US/10/037,340
CURRENT FILING DATE: 2002-03-14
PRIOR APPLICATION NUMBER: 60/276,025
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/325,149
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/276,026
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: 60/324,967
PRIOR FILING DATE: 2001/09/26
PRIOR APPLICATION NUMBER: 60/311,732
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: 60/325,102
PRIOR FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 60/323,580
PRIOR FILING DATE: 2001-09-19
NUMBER OF SEQ ID NOS: 363
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 284
LENGTH: 771
TYPE: PRT
ORGANISM: Homo sapiens
US-10-097-340-284

Alignment Scores:
Pred. No.: 0 Length: 771
Score: 4201.00 Matches: 771
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.80% Indels: 0
DB: 14 Gaps: 0

US-09-774-490-1 (1-2709) x US-10-097-340-284 (1-771)
QY 200 ATGGGCTGTTAACTAGGATGCTCTTTCTGGGAGTATTACTTACAGCAGACA 259
DB 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
QY 260 AACTATCAGAATGGGAAGAACAAATGTCCCAAGCTGAAATATATCTCAAAAGAAATGTTG 319
DB 21 AsnTyrGlnAsnGlyLysAsnValProAsgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCAAACATGTGATCATCTTCAATGCTTGGCCAGCAACAGCTCAGATTATCATCTTC 379
DB 41 GluSerAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
QY 380 CTTTTCGATGAGCAACGAGTAGGCTGTATGTTGGAGCAAGGATCACATATTTTCATTC 439
DB 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGTTAATATCAAGATTTTCAAAAGATGTGTGGCCAGTATCTTACACCAAGAAGA 499
DB 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
QY 500 GATGAATGCAAGTGGCTGGAAGACATCTCTGAAGATGCTAAATTTTCATCAAGGTA 559
DB 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATATATCAGACTCATTGTACGCTGTGGAAACGGGGCTTTTCATCCAATT 619
DB 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACTACATTTGAATATGACATCATCTGAGGACATATTTTAAAGCTGGAGAACTCA 679
DB 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTGAACCGGCTGGAGAGTCCATATGACCTTAAGCTGTGACAGCATCCCTT 739
DB 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATGATGGAGAATTATCTCGAAGTGCAGCTGATTTTATGGGGGAGACTTGTCT 799
DB 181 LeuIleAspGlyLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCGGAACCTCTTGGGCAACCAACCAATCAGCAGACAGCAGCATGATTCAGGTGG 859
DB 201 IlePheArgThrLeuGlyHisHisProIleAsgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCAATGATCCAAAGTTTCATTAGTCCCACTCATCTCAGAGAGTGACAATCTCTGAAAGT 919
DB 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATATCTTTCTTCGTTGAATGAAATAGATGGAAGACACATCTCTGAAAGCT 979
DB 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ACTCAGCTAGATAGTATGCAAGAATGACTTTTGGAGGGCACAAGAAGTCTGGTG 1039
DB 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
QY 1040 AATAAATGACAAACATCTCTCAAGCTCTGTGATTTGCTCAGTCCAGGTCCTAATGGC 1099
DB 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
QY 1100 ATTGACACTCATTTTGTGATGAACTGCAGGATGATTCCTAATCAACTTTTAAAGATCTTAA 1159
DB 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
QY 1160 AATCCAGTTGTATATGAGTGTTCACACTTCCAGTAAACATTTTCAAGGGATCAGCCGTG 1219
DB 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
QY 1220 TGTATGTATAGCATGATGATGTGAGAGGGTCTCTCTGTTGGTCCATATCCACAGGGAT 1279
DB 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360
QY 1280 GGAACCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTATCCAGGCCAGGAAT 1339
DB 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
QY 1340 TGTCCCGCAAAACATTTGGTGTGTTGACTCTACAAGAGACCTTCTCATGATGTATA 1399
DB 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspValIle 400
QY 1400 ACCTTTGCAAGAAGTCAATCCAGCATGTACAAATCCAGTGTTCCTATGAACAAATCGCCA 1459
DB 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
QY 1460 ATAGTGATCAAAACGGATGTAAATTTCAATTTTACAAATTTGCTAGACCGAGTGGAT 1519
DB 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
QY 1520 GCAGAGATGCAGATGATGATGTTTATCGGAACAGATGTTGGGACCGTCTTATAA 1579
DB 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
QY 1580 GTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGATTAGAGAGGTTCTGCTGGAAGAAATG 1639
DB 461 ValValSerIleProLysGluThrTyrAspLeuGluGluValLeuLeuGluMet 480
QY 1640 ACAGTTTTCGGNACCGACTGCTATTCAGCAATGAGCTTTCCTACTAAGCAGCAACAA 1699
DB 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGlnGln 500
QY 1700 CTATATATTTGGTTCAACGGCTGGGGTTGCCAGCTCCCTTTACACCGGTGTGATATTAC 1759
DB 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
QY 1760 GGGAAACCGTGTCTGAGTGTTCCTCGCCGAGACCTTACTGCTGCTGGGATGCTTCT 1819
DB 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
QY 1820 GCATGTTCTCGCTATTTTCCACTCCAAAGAGACGACAGCAGCAAGATATAGAAT 1879
DB 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560

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QY 1880 GGAGACCCACTGACTCTGTTTACAGCTTACACCATGATTAATCAACATGGCCACAGCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro 580
QY 1940 GAAGAGAGATCATCTATCGTCTAGAGATAGTACACATTTTTCGAATGCAAGTCCGAAG 1999
Db 581 GluGluArgGilellellyrGlyValGluAsnSerSerThrPheLeuGluCysSerProlys 600
QY 2000 TGCAGAGAGCGCTGCTCTATTGGCAATTCCAGAGCGGAAATGAAGAGCGAAAGAGAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArglysGluGlu 620
QY 2060 ATCAGAGTGGATGATCATATCATCAGGACAGATCAAGCCCTTCTGCTAGTACTACAA 2119
Db 621 IleArgValAspAspHisIlelleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
QY 2120 CAGAAGCATTCAGGCAATTACCTCTGCCATGGCTGGAAACATGGGTTCATACAAACTCTT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
QY 2180 CTTAAGTTAACCTGGAGTCTATGACACAGAGCATTTGGAAGAACTTCTTCTATTAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
QY 2240 GATGATGGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCCAGAAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
QY 2300 GTCTGTACAGAGACTTCATGACGCTCATCAACACCCCAATCTCAACACGATGATGAG 2359
Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
QY 2360 TTCTGTGAACAGTTTGGAAAGGACCGAAACACACGTCGGCAAGGCCAGGACATACC 2419
Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
QY 2420 CCAGGGAACAGTAACAAATGGAGACACTTACAGAAATAAGAAAGGTAGAAACAGGAGG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
QY 2480 ACCACGAATTTGAGAGGGACCCAGGAGTGTC 2512
Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 2
US-10-262-538-10
; Sequence 10, Application US/10262538
; Publication No. US20030113324A1
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: NEUROFILIN/VEGF-C/VEGFR-3 MATERIALS AND METHODS
; FILE REFERENCE: 28967/37564
; CURRENT APPLICATION NUMBER: US/10/262,538
; CURRENT FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 771
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-262-538-10

Alignment Scores:
Pred. No.: 0 Length: 771
Score: 4201.00 Matches: 771
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.80% Indels: 0
DB: 14 Gaps: 0

US-09-774-490-1 (1-2709) x US-10-262-538-10 (1-771)
QY 200 ATGGGCTGGTAACTAGGATGTCGTCTTTCTGGGGAGTATTACTTACAGCAGAGCA 259
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Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
QY 260 AACTATCAGAAATGGGAAGAAACAATGTCCCAAGGCTGAAATATCTCTCAACAAGAAATTTTG 319
Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCCAACAATGTGATCATCTTCATGGCTTGGCCAAACAGCTCCAGTTCATACCTTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerSerTyrHisThrPhe 60
QY 380 CTTTGTGATGAGGAACCGAGTAGGCTGTATGTTGGACAAAGGATCACATATTTTCATTC 439
Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGGTTAATATCAAGGATTTTCAAAAGATTGTGTGGCCAGTATCTTACACCAGAAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
QY 500 GATCAATGCAAGTGGGCTGGAAAGACATCTCTGAAGAATGTGCTAATTTTCATCAAGGTA 559
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATATCAGACTCACTTGTAGCCCTGTGGAACGGGGGCTTTTTCATCCAAT 619
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QY 620 TGCACCTACATTGAAATGGACATCATCTCGAGACAATATTTTAAGCTGGAGAACTCA 679
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QY 680 CATTTTCAAAACGGCGCTGGGAAGAGTCCATATCACCTTAAGCTGTGACAGCATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGAGAAATATATCTCTGGAACCTGACGCTGATTTTATGGGGCAGACTTCCT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCGGAACCTTTGGGCACCCACCACCAATCAGGACAGACAGCATGATTTCCAGGTGG 859
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QY 860 CTCAATGATCCAAAGTTTCATTAGTGGCCACCTCATCTCAGAGAGTGACAATCTCTGAAGAT 919
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QY 920 GACAAAGTATATCTTTTCTCCGTGAAATGCAATAGATGGAGNACACTCTGGAAAGCT 979
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QY 980 ACTCACGCTAGATAGGTTCAGATATGCAAGAATGACTTTGGAGGGCACAGAAGTCTGGTG 1039
Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
QY 1040 AATAAATGGACAACATTCCTCAAGCTCGTCTGATTTGCTCAGTGCAGTCCAGTCCAAATGGC 1099
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QY 1160 AATCCAGTTGTATAGGAGTGTTTTACGACTTCCAGTAAACATTTTCAAGGGATCAGCCGTG 1219
Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
QY 1220 TGTATGATAGCATGAGTGTGAGAGGGTGTTCCTTGGTCCATATGCCACAGGAT 1279
Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360
QY 1280 GGACCCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTCTATCCACGGCCAGGAACT 1339
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361 GlyProAsnTyrGlnTrpValProTyrGlnArgValProTyrProArgProGlyThr 380
1340 TGTCACGAGAAACATTTGGTGGTTTACCTCTACAAAGGACCTTCTGTGATGATTATA 1399
381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspValIle 400
1400 ACCTTTGAAGAAGCATCCAGCCATGACAAATCCAGTGTTCCTATGAAACAATCGCCCA 1459
401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
1460 ATAGTATCAAAACCGATGTAATATCAATTAACAATTCGCTAGACCGAGTGGAT 1519
421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspValAsp 440
1520 CGAGAGATGGACATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1579
441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
1580 GTAGTTTCAATTCCTAAGAGACTTGTATGATTTAGAGAGGTTCTGCTGGAAGAAATG 1639
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481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
1700 CTATATATTGGTTCAACGCTGGGTTGCCAGCTCCCTTTACACCGGTGTGATATTAC 1759
501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
1760 GGAAGACGCTGTGCTAGTGTTCCTCGCCGAGACCTTACTGTGCTGGATGGTCT 1819
521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
1820 GCATGTTCTCGCTATTTCCCTACTCGAAGAGACGACCAAGACCAAGATATAGAAAT 1879
541 AlaCysSerArgTyrPheProThrAlaLysArgThrArgGlnAspIleArgAsn 560
1880 GGAGACCCACTGACTGCTTTCAGACTTACACCATGATATACCATGGCCAGCCCT 1939
561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisGlyHisSerPro 580
1940 GAAGAGAGATCATCTATGCTAGATAGATAGATAGATAGATAGATAGATAGATAGAT 1999
581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
2000 TGCAGAGAGCGTGTCTATTGGCAATTCAGAGCGCAATGAAAGACGCAAAAGAGAG 2059
601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620
2060 ATCAGAGTGGATCATCATCATCATCAGACAGATCAAGGCTTCTCTAGTAGTCTACAA 2119
621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
2120 CAGAAGATTACGCAATTAACCTCTGCCATGGGTGGAACTGGTGTTCATACAACTCTT 2179
641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
2180 CTTAAGTAAACCTGGAGTCAATTCAGACAGAGCATTTGGAGAACTTCTCTCATTAAGAT 2239
661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
2240 GATGATGGAGATGGCTCTAAGACCAAGAAATGTCATAGCATCACACCTAGCCAGAG 2299
681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
2300 GTCTGTACAGACTTCTATGAGTCTATCAACACCCCAATCTCAACACGATGATGAG 2359
701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
2360 TTCTGTGAACAGTTTGGAAAGGACCGCAACACACGTCGCAAGCCAGGACATACC 2419
721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740

2420 CCAGGAAACAGTAACAAATGGAAGCACTTACAGAAAAATAGAAAGGTAGAAACAGGAGG 2479
741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
2480 ACCACGAATTTGAGAGGCGACCCAGGAGTGTC 2512
761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 3
US-10-067-632-54
; Sequence 54, Application US/10067632
; Publication No. US20030166849A1
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; Kolodkin, Alex L.
; Matthes, David
; Beatley, David R.
; O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/067,632
; FILING DATE: 04-Feb-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,610
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/835,268
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 54:
US-10-067-632-54

Alignment Scores:
Pred. No.: 0 Length: 771
Score: 4201.00 Matches: 771
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.80% Indels: 0
Gaps: 14
US-09-774-490-1 (1-2709) x US-10-067-632-54 (1-771)

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QY 260 AACTATCAGATGGGAAGAACAAATGTGCGCAAGCGCTGAAATATCTCTACAAAGAAATGTTG 319
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QY 320 GAATCCAAACAATGATCATCTTTCAATGCTTGGCCAAACAGCTCCAGTATCATACCTTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
QY 380 CTTTGGATGAGGAACGGAGTAGGCTGTATGTGGAGCAAGGATCAATATTTTCATTC 439
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QY 500 GATGAATCAAGTGGGCTCGAAAGACATCCCTGAAAGATGTGCTAAATTCATCAAGGTA 559
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QY 560 CTTAAGGCATATAATCAGACTCACTGTACGCTGTGGACCGGGCTTTTCATCCAATT 619
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Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTGAAGACGGCGTGGGAAGAGTCCATATGACCTTAAGCTGTGACAGATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
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QY 1340 TGTCGCCAGCAAAACATTTGGTGGTTTGTACTCTACAAAGGACCTTCTCTGATGTATATA 1399

Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspValIle 400
QY 1400 ACCTTTTCCAAAGAAGTCCATCCAGCCATGTACAATCCAGTGTTCCTATGAACAATCGCCA 1459
Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
QY 1460 ATAGTGATCAAAACCGATGTAAATTTATCAATTTACAAATTTCTGTAGACCGAGTGGAT 1519
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QY 1640 ACAGTTTTTCGGGAACCGACTGTCTATTTCAGCAATGGAGCTTCCACTAAGCAGCAACAA 1699
Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
QY 1700 CTATATATTGTTCAACGGCTGGGTTGCCAGCTCCCTTTTACACCGTGTGTATTTAC 1759
Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
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Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
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Db 541 AlaCysSerArgTyrPheProThrAlaLysArgThrArgArgGlnAspIleArgAsn 560
QY 1880 GGAGACCCACTGACTCACTGTTGAGATTACACCATGATTAATCCATGCCACAGCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisHisGlyHisSerPro 580
QY 1940 GAACAGAGATCATCTATGTGTAGAGATAGTAGACATTTTGGAAATGCAGTCCGAAG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
QY 2000 TCGCAGAGAGCGTGTCTATTGGCAATTCAGAGCGGAAATGAAGAGCGAAAGAGAG 2059
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QY 2300 GTCTGGTACAGAGACTTCATGCGAGCTCATCAACCCCAATCTCAACAGATGGATGAG 2359
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QY 2360 TTCCTGTCAGACAAGTTTGGAAAGGACCGGAAACAACAGCTCGGCAAGCCAGGACATACC 2419
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Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArg 760

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Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 4

US-10-247-671-164

Sequence 164, Application US/10247671

Publication No. US20030194721A1

GENERAL INFORMATION:

APPLICANT: Mikita, Thomas

APPLICANT: Shiffman, Dov

APPLICANT: Porter, Gordon, J.

APPLICANT: Kaser, Matthew R.

FILE REFERENCE: PA-0050 US

TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS

CURRENT APPLICATION NUMBER: US/10/247,671

CURRENT FILING DATE: 2002-09-18

PRIOR APPLICATION NUMBER: 60/323,784

PRIOR FILING DATE: 2001-09-19

NUMBER OF SEQ ID NOS: 186

SOFTWARE: PERL Program

SEQ ID NO 164

LENGTH: 771

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc feature

OTHER INFORMATION: Incyte ID No. US20030194721A1 1930967CD1

US-10-247-671-164

Alignment Scores:

Pred. No.: 0 Length: 771

Score: 4201.00 Matches: 771

Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0

Query Match: 85.80% Indels: 0

DB: 14 Gaps: 0

US-09-774-490-1 (1-2709) x US-10-247-671-164 (1-771)

QY 200 ATGGCTGTTAACTAGATTCTCTGCTTTCTGGGAGTATTACTTACAGCAGACGA 259

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QY 380 CTTTGGATGAGAACGGAGTAGGCTGTATGTTGGAGCAAGATCATATTTTCATTC 439

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QY 500 GATGATGAGTGGCTGGAAAGACATCTCTGAAGATGCTGAATTTTCATCAAGTA 559

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QY 680 CATTTTGAAAACGGCCGTGGGAAGAGTCCATATGACCTTAAGCTGCTCACACATCCCTT 739

Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180

QY 740 TTAATAGATGGAGAATTATCTCTGAACTGAGCTGATTTTATGGGGCGAGACTTTCCT 799

Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200

QY 800 ATCTTCGGAACCTTGGGACACCAACCACTCAGACAGACAGCAGCATGATTCAGAGTGG 859

Db 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220

QY 860 CTCAATGATCCAAAGTTTCAATAGTCCCACTCATCTCAGAGAGTGACAACTCTGAAGAT 919

Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240

QY 920 GACAAAGTATATCTTTCTTCGTAAGTCAATAGTGGAGACACTCTCGAAAGACT 979

Db 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260

QY 980 ACTCAGCTAGAAATAGTCAAGATATGCAAGATGACTTTGGAGGCGACAGAGTCTGGT 1039

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Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400

QY 1400 ACCTTTGCAAGAGTCACTCAGCCATGTACAATCCAGTGTTCCTATGAACTCCGCCA 1459

Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420

QY 1460 ATAGTGATCAAAACGAGTGTAAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1519

Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440

QY 1520 GCAGAGATGGACAGATGATGTATGTTTATCGGAACAGATGTTGGGACCGCTTCTTAA 1579

Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460

QY 1580 GTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAGAGGTTCTGCTGGAAGAAATG 1639

Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluGluValLeuLeuGluMet 480

QY 1640 ACAGTTTTCGGAAACCGACTGATTTTCAGAAATGGAGCTTCCACTAAGCAGACAA 1699

Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGlnGln 500

QY 1700 CTATATATTGGTTCAACGGCTGGGGTGGCCAGCTCCCTTTACCGGTGTGATATTAC 1759

Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520

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QY 1760 GGGAAAGCGTGTCTGAGTGTGCTCGCCGAGACCTTACTGTGCTTGGAGTGTCT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
QY 1820 GCATGTTCTCGGTATTTTCCCACTCAAGAGACACCAAGACGACGAAGATATAGAAT 1879
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgGThrArgGlnAspIleArgAsn 560
QY 1880 GGAGACCCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro 580
QY 1940 GAAGAGAGAAATCATCTATGCTGTAGAGATAGTAGACATATTTTGGAAATGCGAGTCCGAG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
QY 2000 TCGAGAGAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620
QY 2060 ATCAGAGTGGATGATCATATCATCATCAGGACAGATCAAGGCTTCTGCTAGTACTACAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
QY 2120 CAGAAGGATTCAGGCAATTAACCTCTGCCATGCGGTGGAACATGCGTTTCATACAAACTCT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
QY 2180 CTTAAGGTAACTGGAAGTCACTGACACAGAGCATTTGGAAGAACTTCTTCATAAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuHisLysAsp 680
QY 2240 GATGATGGAGATGGCTTCAAGACCAAGAAATGTCCAATAGCATGACACCTAGCCAGAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
QY 2300 GTCTGTGACAGACTTCATGAGCTCATCAACCCCACTCAACCCCACTCAACCCAGATGATGAG 2359
Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
QY 2360 TTCTGTGACAACTTTGGAAGAGGACCCGAAACACACGTCGCGCAAGGCGCAGCATACC 2419
Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
QY 2420 CCAGGGAACAGTAACAAATGGAAGCACTTACAGAAATACAGAAATGGAAGGAGGAGG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGlnAsnLysLysGlyArgAsnArg 760
QY 2480 ACCACGAATTTGAGAGGCGCCAGGAGTGC 2512
Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

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RESULT 5

US-10-320-769-3

Sequence 3, Application US/10320769

Publication No. US20030158402A1

GENERAL INFORMATION:

APPLICANT: HALL, Kathryn T.

APPLICANT: FREEMAN, Gordon J.

APPLICANT: SCHULTZE, Joachim L.

APPLICANT: BOUSSONIS, Vassiliki

APPLICANT: NADLER, Lee M.

TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES

FILE REFERENCE: DFN-005CPA2,

CURRENT APPLICATION NUMBER: US/10/320,769

PRIOR FILING DATE: 2002-12-16

PRIOR FILING DATE: 1995-11-09

NUMBER OF SEQ ID NOS: 7

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 3

LENGTH: 655

TYPE: PRT

ORGANISM: Homo sapiens

US-10-320-769-3

Alignment Scores:

Pred. No.: 0

Score: 3568.00

Percent Similarity: 100.00%

Best Local Similarity: 100.00%

Query Match: 72.88%

DB: 14

Length: 655

Matches: 655

Conservative: 0

Mismatches: 0

Indels: 0

Gaps: 0

US-09-774-490-1 (1-2709) x US-10-320-769-3 (1-655)

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QY 200 ATGGCTGGTAACTAGGATGTCTGCTTTCTGGGAGTATTACTTACAGCAAGACA 259
Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
QY 260 AACTATCAGAAATGGGAAGAACAATGTGCCAAGCTGAAATATCTCTACAAGAAATGTTG 319
Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCCAACATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATACCTTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerSerTyrHisThrPhe 60
QY 380 CTTTGGATGAGGAACCGAGTAGCTGTATGTGGAGCAAGGATCATATTTTCAATTC 439
Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGTTTAAATCAAGGATTTTCAAAAGATGTGTGGCCAGTATCTTACACCAGAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpValSerTyrThrArgArg 100
QY 500 GATCAATGCAAGTGGGTGGAAAAAGACATCTCTGAGGACAAATATTTTAAAGCTGGAGAACTCA 559
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATATCAGACTCACTTGTAGCTGTGAGCAAGGGGCTTTTCATCCAAAT 619
Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTACATTTGAAATGGACATCATCTCTGAGGACAAATATTTTAAAGCTGGAGAACTCA 679
Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTGAACACCGCCCTGGGAAGAGTCCATATGACCCCTAAGCTGTGACAGCATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGGAGAATTATATCTCTGGAACCTGCGAGTGTATTTATGGGCGGAGACTTTTGT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCCGAACCTTGGGCGACCCACCACCAATCAGGACAGACAGCATGATTCCAGGTGG 859
Db 201 IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCATATGATCCAAAGTTTCATAGTGGCCCACTCATCTCTCAGAGAGTGACATCTCAGAGAT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATATCTTTTCTCCGTGAAATATGCAATAGATGAGAACCACTCTCTGGAAGAACT 979
Db 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ACTCAGCGCTAGAAATAGTCTAGATATGCAAGATGACATTTGGAGGGCACAGAGTCTGGTG 1039
Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
QY 1040 AATAAATGGACAACATCTCTCAAGCTCGTCTGATTTTGTCTCAGTGCAGGTCCTCAATGGC 1099
Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300

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us-09-774-490-1.rapb

Thu Sep 23 08:54:06 2004

QY 1100 ATTGACACTCATTGATGAAGTGGAGTGTATCTCTAATGAACCTTTAAGATCCTAAA 1159
Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
QY 1160 AATCCAGTTGTATATGGAGTGTATACGACTTCCAGTAACTTTCAAGGGATCAGCCGTG 1219
Db 321 AsnProValValTyrGlyValPheThrSerSerAsnIlePheLysGlySerAlaVal 340
QY 1220 TGTATGTATAGCATGAGTGTAGAGAGGGTGTCTCTGTGTCATATGCCACAGGAT 1279
Db 341 CysMetTyrSerMetSerAspValArgArgValPheLeuGlyProTyrAlaHisArgAsp 360
QY 1280 GGACCCCACTATCAATGGTGCTTATCAAGAGAGTCCCTATCCACGCCCAGGAACT 1339
Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
QY 1340 TGTCCACGAAACATTTGGTGGTTTTCACCTCTACAAAGGACCTTCTCTGATGTTTATA 1399
Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400
QY 1400 ACCTTTGCAGAGTCAATCCAGCCATGACATCCAGTGTTCCTATCAACAATCGCCA 1459
Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnArgPro 420
QY 1460 ATAGTATCAAAACGGATGTAATATCAATATCAAAATTTACAAATTTGCTAGACCGAGTGGAT 1519
Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
QY 1520 GGAGAGATGACATGATGTTATGTTATCGAACAGATGTGGACCGTCTTAAA 1579
Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
QY 1580 GTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAGAGTGTCTCTCGAAGAATG 1639
Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluLys 480
QY 1640 ACAGTTTTCGGAACCGACTGCTATTTACAGAAATGGAGCTTTCACATGACGACACAA 1699
Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
QY 1700 CTATATATGTTCAACGCTGGGTTCGCCAGTCCCTTTACACCGGTGTGATTTAC 1759
Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
QY 1760 GGAAGAGCTGTGCTCAGTGTTCCTCGCCGAGACCCCTTACTGTGCTGGATGGTCT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
QY 1820 GCATGTTCTCGTATTTTCCACTGCAAGAGACGACACAGACAGATATAGAAAT 1879
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560
QY 1880 GGAGACCCACTGACTGCTTTCAGACTTACACATGATATACCATGGCCACAGCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisHisGlyHisSerPro 580
QY 1940 GAAGAGAGATCATCTATGCTGTAGATAGTACACATTTTGGATGAGTCCGAG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
QY 2000 TCGCAGAGACGCTGTCTATTGGCAATTCAGAGCGCAATTAAGAGCGCAAGAGAGAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgGlnGluArgLysGluGlu 620
QY 2060 ATCAGAGTGCATGATCATATCATCAGACAGATCAAGCGCTTCTCTAGTGTCTACAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
QY 2120 CAGAGGATTCAGGCAATTAACCTCTGCCATGGGTGGAACATGGG 2164
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGly 655

US-09-946-374-310
Sequence 310, Application US/09946374
Publication No. US20030073129A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gao, Wei-Qiang
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, Christopher J.
APPLICANT: Gurney, Austin L.
APPLICANT: Hillan, Kenneth J.
APPLICANT: Fan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Smith, Victoria
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2830P1C1
CURRENT APPLICATION NUMBER: US/09/946,374
CURRENT FILING DATE: 2001-09-04
PRIOR APPLICATION NUMBER: 60/098716
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098723
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098749
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098750
PRIOR FILING DATE: 1998-09-01
PRIOR APPLICATION NUMBER: 60/098803
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098821
PRIOR FILING DATE: 1998-09-02
PRIOR APPLICATION NUMBER: 60/098843
PRIOR FILING DATE: 1998-09-02
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PRIOR APPLICATION NUMBER: 60/099602
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099642
PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099741
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099754
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PRIOR APPLICATION NUMBER: 60/099812
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099815
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/099816
PRIOR FILING DATE: 1998-09-10
PRIOR APPLICATION NUMBER: 60/100385
PRIOR FILING DATE: 1998-09-15
PRIOR APPLICATION NUMBER: 60/100388

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/ PRIOR FILING DATE: 1998-09-15
/ PRIOR APPLICATION NUMBER: 60/100390
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/ PRIOR APPLICATION NUMBER: 60/100584
/ PRIOR FILING DATE: 1998-09-16
/ PRIOR APPLICATION NUMBER: 60/100627
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/ PRIOR APPLICATION NUMBER: 60/100664
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/ PRIOR APPLICATION NUMBER: 60/100684
/ PRIOR FILING DATE: 1998-09-17
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/ PRIOR FILING DATE: 1998-09-17
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/ PRIOR FILING DATE: 1998-09-17
/ PRIOR APPLICATION NUMBER: 60/100848
/ PRIOR FILING DATE: 1998-09-18
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/ PRIOR FILING DATE: 1998-09-18
/ PRIOR APPLICATION NUMBER: 60/100919
/ PRIOR FILING DATE: 1998-09-17
/ PRIOR APPLICATION NUMBER: 60/100930
/ PRIOR FILING DATE: 1998-09-17
/ PRIOR APPLICATION NUMBER: 60/101014
/ PRIOR FILING DATE: 1998-09-18
/ PRIOR APPLICATION NUMBER: 60/101068
/ PRIOR FILING DATE: 1998-09-18
/ PRIOR APPLICATION NUMBER: 60/101071
/ PRIOR FILING DATE: 1998-09-18
/ PRIOR APPLICATION NUMBER: 60/101279
/ PRIOR FILING DATE: 1998-09-22
/ PRIOR APPLICATION NUMBER: 60/101471
/ PRIOR FILING DATE: 1998-09-23
/ PRIOR APPLICATION NUMBER: 60/101472
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/ PRIOR APPLICATION NUMBER: 60/101474
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/ PRIOR FILING DATE: 1998-09-23
/ PRIOR APPLICATION NUMBER: 60/101738
/ PRIOR FILING DATE: 1998-09-24
/ PRIOR APPLICATION NUMBER: 60/101741
/ PRIOR FILING DATE: 1998-09-24
/ PRIOR APPLICATION NUMBER: 60/101743
/ PRIOR FILING DATE: 1998-09-24
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/ PRIOR FILING DATE: 1998-09-24
/ PRIOR APPLICATION NUMBER: 60/101916
/ PRIOR FILING DATE: 1998-09-24
/ PRIOR APPLICATION NUMBER: 60/102207
/ PRIOR FILING DATE: 1998-09-29
/ PRIOR APPLICATION NUMBER: 60/102240
/ PRIOR FILING DATE: 1998-09-29
/ PRIOR APPLICATION NUMBER: 60/102307
/ PRIOR FILING DATE: 1998-09-29
/ PRIOR APPLICATION NUMBER: 60/102330
/ PRIOR FILING DATE: 1998-09-29
/ PRIOR APPLICATION NUMBER: 60/102331
/ PRIOR FILING DATE: 1998-09-29
/ PRIOR APPLICATION NUMBER: 60/102484
/ PRIOR FILING DATE: 1998-09-30

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Alignment Scores:
Pred. No.: 1.9e-201
Score: 2245.50
Percent Similarity: 73.67%
Best Local Similarity: 54.92%
Query Match: 45.86%
DB: 10
Length: 777
Matches: 413
Conservative: 141
Mismatch: 177
Indels: 21
Gaps: 9

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US-09-774-490-1 (1-2709) x US-09-946-374-310 (1-777)

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QY 275 AAGAACATGCGCAAGCTGAATTATCTACAAAGAAATGTTGAATCCAAATGTG 334
Db 39 LysGlnAsnIleProArgLeuLysLeuThrTyrlsAspleuLeuLeuSerAsnSerCys 58
QY 335 ATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCATACCTTCTTTTGGATGAGAA 394
Db 59 IleProPheLeuGlySerSerSerGlyLeuAspPheGlnThrLeuLeuLeuAspGlu 78

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US-10-206-915-348

/ Sequence 348, Application US/10206915
/ Publication No. US20040029221A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Chen, Jian
/ APPLICANT: Desnoyers, Luc
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Pan, James
/ APPLICANT: Smith, Victoria
/ APPLICANT: Watanabe, Colin K.
/ APPLICANT: Wood, William I.
/ APPLICANT: Zhang, Zemin

/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
/ FILE OF INVENTION: ACIDS ENCODING THE SAME

/ FILE REFERENCE: P34301C13

/ CURRENT APPLICATION NUMBER: US/10/206,915

/ CURRENT FILING DATE: 2002-07-26

/ PRIOR APPLICATION NUMBER: 10/052586

/ PRIOR FILING DATE: 2002-01-15

/ PRIOR APPLICATION NUMBER: 60/059263

/ PRIOR FILING DATE: 1997-09-18

/ PRIOR APPLICATION NUMBER: 60/059266

/ PRIOR FILING DATE: 1997-09-18

/ PRIOR APPLICATION NUMBER: 60/062250

/ PRIOR FILING DATE: 1997-10-17

/ PRIOR APPLICATION NUMBER: 60/063120

/ PRIOR FILING DATE: 1997-10-24

/ PRIOR APPLICATION NUMBER: 60/063121

/ PRIOR FILING DATE: 1997-10-24

/ PRIOR APPLICATION NUMBER: 60/063486

/ PRIOR FILING DATE: 1997-10-21

/ PRIOR APPLICATION NUMBER: 60/063540

/ PRIOR FILING DATE: 1997-10-28

/ PRIOR APPLICATION NUMBER: 60/063541

/ PRIOR FILING DATE: 1997-10-28

/ PRIOR APPLICATION NUMBER: 60/063544

/ PRIOR FILING DATE: 1997-10-28

/ PRIOR Application data removed - See File Wrapper or PALM.

/ NUMBER OF SEQ ID NOS: 612

/ SEQ ID NO 348

/ LENGTH: 777

/ TYPE: PRT

/ ORGANISM: Homo Sapien

US-10-206-915-348

Alignment Scores:
Pred. No.: 1.9e-201 Length: 777
Score: 2245.50 Matches: 413
Percent Similarity: 73.67% Conservative: 141
Best Local Similarity: 54.92% Mismatches: 177
Query Match: 45.86% Indels: 21
DB: 12 Gaps: 9

US-09-774-490-1 (1-2709) x US-10-206-915-348 (1-777)

QY 275 AAGAACATGTGCCAGGCTGAATATCTCAAGAAATGTTGGAATCCACAAATGTG 334
Db 39 LysGlnAsnIleProArgLeuLysLeuThrTyrLysAspLeuLeuSerAsnSerCys 58
QY 335 ATCACTTTCAATGGTGGCCCAACAGCTCCAGTTATCATACCTCTCTTTTGGATCAGGAA 394
Db 59 IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuLeuAspGluGlu 78
QY 395 CGAGTAGCTGTATGTGGCAAGATCAATATTTTCAATCGACTGGTTAAATATC 454
Db 79 ArgGlyArgLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu 98
QY 455 ---AAGGATTTTCAAAAGATTTGTGGCCAGATCTTACACCAAGAGAGATCAATGCAAG 511
Db 99 AsnLysAsnPheLysIleIleTyrTrpProAlaAlaLysGluArgValGluLeuLys 118

QY 512 TGGGCTGGAAGAAGACATCTCTGAAGAATGTCTAATTTCAATCAAGGTACTTAAGGCATAT 571
Db 119 LeuAlaGlyLysAspAlaAenThrGluCysAlaAsnPheIleArgValLeuGlnProTyr 138
QY 572 AATCAGACTCATTGTAGCGCTGTGGAAACGGGGCTTTTTCATCCAATTTGCACCTACATT 631
Db 139 AsnLysThrHisIleTyrValCysGlyThrGlyAlaPheHisProIleCysGlyTyrIle 158
QY 632 GAAATTTGGACATCATCTCGAGCAATATTTTAAAGCTGGGAGAACTCACATTTTGAAC 691
Db 159 AspLeuGlyValTyrLysGluAspIleIlePheLysLeuAspThrHisAsnLeuGluSer 178
QY 692 GCGCTGGGAAGAGTCCATATGACCTAAGCTGTGACAGCATCCCTTTTAAATAGATCGA 751
Db 179 GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu 198
QY 752 GAATTTACTCTGGAATCGAGCTGATTTTATGGGGGAGACTTTGTATCTTCCGAACT 811
Db 199 TyrLeuTyrSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218
QY 812 CTTGGG-----CACCAACCCCAATCAGGACAGCAGCATGATCCAGGTGCTC 862
Db 219 LeuGlyProThrHisAspHisHisTyrIleArgThrAspIleSerGluHisTyrTrpLeu 238
QY 863 AATGATCCAAAGTTTATTAGTGGCCACTCATCTCAGAGAGTGAACAATCTCTGAAGATGAC 922
Db 239 AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAsp 258
QY 923 AAGTATATCTTTTCTTCGTTGAAATGCAATAGATGAGAACTCTCTGGAAGCTACT 982
Db 259 LysIleTyrPhePheArgGluSerSerGlnGluGlySerThrSerAspLysThrIle 278
QY 983 CACCTAGAATAGTTCAGATATGCAAGAATGACTTTTGGAGGGCACAGAACTCTGCTGAAT 1042
Db 279 LeuSerArgValGlyArgValCysLysAsnAspValGlyGlyGlnArgSerLeuIleAsn 298
QY 1043 AAATGGACAACATCTCTCAAGCTCTGCTGATTTGCTCAGTGCAGGTGCAAAATGGGATT 1102
Db 299 LysTrpThrThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla 318
QY 1103 GACACTCATTTTGAATGAATGCAAGATGATTTCTTAATGAATTTAAAGATCTCTAAAAT 1162
Db 319 AspThrTyrPheAspGluLeuGlnAspIleTyrLeuLeuProThrArgAspGluArgAsn 338
QY 1163 CCAGTTGTATGAGGTGTTTACACTTCAGTAACATTTTCAAGGATCAGCGGTGTGT 1222
Db 339 ProValValTyrGlyValPheThrThrSerSerIlePheLysGlySerAlaValCys 358
QY 1223 ATGTATAGCATGATGTGAGAAGGTGTTCTTGTGTCATATCCACACAGGATGGA 1282
Db 359 ValTyrSerMetAlaAspIleArgAlaValPheAsnGlyProTyrAlaHisLysGluSer 378
QY 1283 CCCAATCATCAATGGGTGCTTATCAAGGAAGAGTCCCTTATCCAGCGCCAGGAATTTGT 1342
Db 379 AlaAspHisArgTrpValGlnTyrAspGlyArgIleProTyrProArgProGlyThrCys 398
QY 1343 CCCAGCAAAACATTTTGGTGT---TTTGACTCTCAAAAGGACCTTCTGTGATGTATATA 1399
Db 399 ProSerLysThrTyrAspProLeuIleLysSerThrArgAspPheProAspValIle 418
QY 1400 ACCTTTTCAAGAAGTATCCAGCCATGTACAAATCCAGTGTTCCTATGAACAATCGCCCA 1459
Db 419 SerPheIleLysArgHisSerValMetTyrLysSerValTyrProValAlaGlyGlyPro 438
QY 1460 ATAGTATCAAAACGGATGTAATTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1519
Db 439 ThrPheLysArgIleAsnValAspTyrArgLeuThrGlnIleValValAspHisValIle 458
QY 1520 GCAGAGATGCGACAGATGATGTTTATCGGAACAGATGTTGCGGCGGCTCTTAA 1579
Db 459 AlaGluAspGlyGlnTyrAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys 478

QY 1580 GTAGTTTCAATTCCTAAGGACCTTGATGATTAGAGAGGCTTCTGCTGGAAGAAATG 1639
 Db ValValserIleSerLysGluLysTrp--AsnMetGluValValLeuGluGluLeu 497
 QY 1640 ACAGTTTTCGGGAACCGACGCTGATTTACGCAATGAGCTTCCACTAAGCAGCAACA 1699
 Db GlnIlePheLysHisSerIleLeuLeuMetGluLeuSerLeuLysGlnGln 517
 QY 1700 CTATATATGTTTCAACCGCTGGGTTGCCAGCTCCCTTACACCGGTTGATATTAC 1759
 Db LeuTyrlleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTy 537
 QY 1760 GGGAAAGCTGCTGAGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1819
 Db GlyLysAlaCysAlaAspCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlyAsn 557
 QY 1820 GCATGTTCTCGCTATTTTCCACTGCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 1879
 Db AlaCysSerArgTyrAlaProThrSerLysArgArgAlaArgGlnAspValLysTyr 577
 QY 1880 GGACACCCACGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1939
 Db GlyAspProIleThrGlnCysTrpAspIleLeuSerIleSerHis---GluThrAla 596
 QY 1940 GAACAGAGAAATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1999
 Db AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys 616
 QY 2000 TCGCAGAGAGCTGGTCTATTTGCAATTCAGAGCGGAATTAAGAGAGAGAGAGAG 2059
 Db SerGlnGlnAlaThrIleLysTyrTrpIleGlnArgSerGlyAspGluHisArgGluGlu 636
 QY 2060 ATCAGAGTGGATGATATATCATCAGCAGAGATCAAGGCTTCTGCTAGTGTCTACAA 2119
 Db LeuLysProAspGluArgIleLysLysThrGluTyrlleLeuLeuLysSerLeuGln 656
 QY 2120 CAGAAGATTCAGCAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2179
 Db LysLysAspSerGlyMetTyrCysLysAlaGlnGluHisThrPheIleHisThrIle 676
 QY 2180 CTTAAGGTAACTTCGGAAGTCATTCAGCAGAGATTCGGAAGACTTCTTCATAAGAT 2239
 Db ValLysLeuThrLeuAsnValIleGluAsnGluLysMetGluAsnThrGlnArgAlaGlu 696
 QY 2240 GATGATGGAGAGCTCTATAGCAACAAAGAAATGCTCAATAGCATACACCTTACCC 2299
 Db HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg 710
 QY 2300 GTCTGCTACAGACTTCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 2359
 Db LeuArgTyrLysAspTyrIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln 729
 QY 2360 TCTGCTGAAACAGTTTGGAAAGAGGACCGGAACAAACAGCTCGCAAGAGCCAGGAC 2419
 Db TyrCysGluGlnMetTrpHisArgGluLysArgGlnArgAsnLysGlyGly----- 747
 QY 2420 CCAGGGAACAGTAACTAAGTGAAGCACTTACAGAAATAAGAAAGGTAGAAACAGGAG 2479
 Db ProlLysTrpLysHisMetGlnGluMetLysLysLysArgAsnArgArg 763
 QY 2480 ACCAC---GAATTTGAGAGGGCACCAGGAGTGC 2512
 Db HisArgAspLeuAspGluLeuProArgAlaVal 775

RESULT 8

US-10-199-670-348
 ; Sequence 348, Application US/10199670
 ; Publication No. US20040033560A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
 APPLICANT: Gurney, Austin L.
 APPLICANT: Pan, James
 APPLICANT: Smith, Victoria
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 FILE REFERENCE: P3430R1C401
 CURRENT APPLICATION NUMBER: US/10/199,670
 CURRENT FILING DATE: 2002-07-19
 PRIOR APPLICATION NUMBER: 10/052586
 PRIOR FILING DATE: 2002-01-15
 PRIOR APPLICATION NUMBER: 60/059263
 PRIOR FILING DATE: 1997-09-18
 PRIOR APPLICATION NUMBER: 60/059266
 PRIOR FILING DATE: 1997-09-18
 PRIOR APPLICATION NUMBER: 60/062250
 PRIOR FILING DATE: 1997-10-17
 PRIOR APPLICATION NUMBER: 60/063120
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/063121
 PRIOR FILING DATE: 1997-10-24
 PRIOR APPLICATION NUMBER: 60/063486
 PRIOR FILING DATE: 1997-10-21
 PRIOR APPLICATION NUMBER: 60/063540
 PRIOR FILING DATE: 1997-10-28
 PRIOR APPLICATION NUMBER: 60/063541
 PRIOR FILING DATE: 1997-10-28
 PRIOR APPLICATION NUMBER: 60/063544
 PRIOR FILING DATE: 1997-10-28
 PRIOR APPLICATION data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 612
 SEQ ID NO 348
 LENGTH: 777
 TYPE: PRT
 ORGANISM: Homo Sapien
 US-10-199-670-348

Alignment Scores:
 Pred. No.: 1,9e-201 Length: 777
 Score: 2245.50 Matches: 413
 Percent Similarity: 73.67% Conservative: 141
 Best Local Similarity: 54.92% Mismatches: 177
 Query Match: 45.86% Indels: 21
 DB: 12 Gaps: 9

US-09-774-490-1 (1-2709) x US-10-199-670-348 (1-777)
 QY 275 AGAACAATGTCCTGAGCTGAAATATCTTACAAAGAAATGTTGGAATCCAAATGTG 334
 Db 39 LysGlnAsnIleProArgLeuLysLeuThrTyrLysAspLeuLeuSerAsnSerCys 58
 QY 335 ATCACTTTCAATGGCTTGGCCCAACAGCTCCAGTTATCATACCTTCCTTTTGGATGAGAA 394
 Db 59 IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuAspGluGlu 78
 QY 395 CGAGTAGCTGTATGTTGGAGCAAGAGATCACAATATTTTCATTCGACCTGGTTATATC 454
 Db 79 ArgGlyArgLeuLeuLeuGlyAlaLysAspHisIlePheLeuSerLeuValAspLeu 98
 QY 455 ---AAGGATTTTCAAAGATTTGTCGCCAGTATCTTACACCAAGAGAGATGAATCCAAG 511
 Db 99 AsnLysAsnPheLysLysIleTyrTrpProAlaAlaLysGluArgValGluLeuLysLys 118
 QY 512 TCGGCTGGAAGACATCTGGAAGATGCTGTAATTCATCAAGTACTTAAAGGCATAT 571
 Db 119 LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPheIleArgValLeuGlnProTyr 138
 QY 572 AATCAGACTCACTGTACGCTGTGGAGCGGGCTTTTTCATCAATTTCCACTACATT 631
 Db 139 AsnLysThrHisIleTyrValCysGlyThrGlyAlaPheHisProIleCysGlyTyrIle 158

632 GAAATTGGACATCATCTCGAGACACAATAATTTTAAAGCTGGGAGAACTCACATTTTGAAAAC 691
Db : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
159 AspLeuGlyValTy rLysGl uAspIleilePheLysLeuAspThrHisAsnLeuGluSer 178
QY 692 GCCGTGGGAAGAGTCATATGACCACTAAGCTGCTGCAGCAGCATCCCTTTTAATAGATGGA 751
Db : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
179 GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu 198
QY 752 GAATTATACTCTCGAACTGCCAGCTGATTTTATGGGGCGAGACTTTGCTATCTTCCCGAACT 811
Db : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
199 TyrLeuTy rSerGlyTh rAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218
QY 812 CTTCGG-----CACCAACCCAATCAGACAGACAGCAGCATGANTCCAGGTGCTC 862
Db : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
219 LeuGlyProThrHisAspHisH i sTyrIleArgThrAspIleSerGluHisTyrTrpLeu 238
QY 863 AATGATCCAAAGTTTCATTAGTGCACCCTCATCTCAGAGATGACAATCTCGAAGATGAC 922
Db : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
239 AsnGlyAlaLysPheIleGlyTh rPhePheIleProaspThrTy rAsnP roAspAsp 258
QY 923 AAAGTATACTTTTCTCCGTGAANAATGCAATAGATGAGAACACTCTGGAAAAGCTPACT 982
Db : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
259 LysIleTy rPhePheArgGluSerSerGlnGluGlySerThrSerAspLysThrIle 278
QY 983 CACGCTAGAATAGTTCAGATATCAAGAAATGACATTTGGAGGGCACAGAACTCTGGTCAAT 1042
Db : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
279 LeuSerArgValGlyArgValCysLysAsnAspValGlyGlyGlnArgSerLeuIleAsn 298
QY 1043 AAATGGACAACATTCCTCAAAGCTCGTCTGATTTGCTCAGTGCAGGCTCCAAATGGCAT 1102
Db : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
299 LysTrpThrThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla 318
QY 1103 GACACTCATTTTGATGAACCTCGAGATGATTCTCTAATGAACCTTAAAGATCTCTAAAAT 1162
Db : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
319 AspThrTy rPheAspGluLeuInasPileTy rLeuLeuProThrArgAspGluuArgAsn 338
QY 1163 CCAGTTGTATAGAGTGTTTACGACTTCAGATTAACATTTTCAAGGATCAGCGCTGTGT 1222
Db : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
339 ProValValTy rGlyValPheThrThrThrSerSerIlePheLysGlySerAlaValCys 358
QY 1223 ATGTATAGCATGATGATGAGNAGGTTCTCTGTCATATGCCACAGGATGGA 1282
Db : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
359 ValTy rSerMetAlaSpIlel eArgAlaValPheAsnGlyProTy rAlaHisLysGluSer 378
QY 1283 CCCAACTCATCAATGGTGCCTTATCAAGGAAGAGTCCCCTATCCAGGCCAGAACTGT 1342
Db : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
379 AlaaspHisargTrpValGlnTy rAspGlyArgIleProTy rProArgProGlyThrCys 398
QY 1343 CCCAGCAAAACATTTGGTGGT---TTTGACTCTACAAAGGACCTTCTGATGATGTATA 1399
Db : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
399 ProSerLysThrTy rAspProLeuIleLysSerThrArgAspPheProAspValIle 418
QY 1400 ACCTTTCCAAAGATCATCCAGCATCTCAATCCAGTGTTCCTATGAACAATCCCCA 1459
Db : --::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
419 SerPheIleLysargHisSerValMetTy rLysSerValTy rProValalaGlyGlyPro 438
QY 1460 ATAGTGATCAAAACGGATGTAATATCAATTTACAAATTCCTAGACCCAGTGGAT 1519
Db : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
439 ThrPheLysArgIleAsnValAspTy rArgLeuThrGlnIleValValAspHisValIle 458
QY 1520 GCAGAGATGCAGATGATGATTGTGTTTTATCGGAACAGATCTCGGACCGTCTCTAAA 1579
Db : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
459 AlagLuaspGlyGlnTy rAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys 478
QY 1580 GTAGTTTCAATTCTAAGGAGACTTGATATGATTTTAGAAGAGGTTCTGCTGGAAGAAATG 1639
Db : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
479 ValValSerIleSerLysGlnLysTrp---AsnMetGluGluValValLeuGluGluLeu 497
QY 1640 ACAGTTTTCGGAAACCGACTGCTATTTCAGCAATGGAGCTTTCCTAAGCAGCAACAA 1699
Db : ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: ::::: :::::
498 GlnIlePheLysHisSerIlelleLeuAsnMetGluLeuSerLeuLysGlnGln 517

QY	1700	CTATATATTGGTTCAACGGCTGGGGTTGCCAGCTCCCTTTACACCGGTGTGATATTTAC	1751
Db	518	LeuTyrIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTyr	537
QY	1760	GGGAAACGGTGTGTAGTGTTCCTCGCCGAGACCCTTACTGTGCTTCGGATGTCTT	1819
Db	538	GlyLysAlaCysAlaAspCysCysLeuAlaArgAspProTyrCysAlaThrPaspGlyAsn	557
QY	1820	GCATGTTCTCGCTATMTTTCACCTGCAAGAGACGCACAAGACATATAAGAAAT	1879
Db	558	AlaCysSerArgTyrAlaProThrSerLysArgAlaArgGlnAspValLysTyr	577
QY	1880	GGAGACCACTGACTCACTGTTCCAGATTTACACCATGATAATCACCATGCCACGCCCT	1939
Db	578	GlyAspProIleThrGlnCysThrPaspIleGlnAspSerIleSerHis---GluThrAla	596
QY	1940	GAGAGAGAAATCATCTATGTGTAGAGATAGTAGACACATTTTTTGAATGCAGTCCGAAG	1999
Db	597	AspGlnLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys	616
QY	2000	TCGCAGAGACGGCTGGTCTATTCGCAATTCAGAGCGGGAATGAAGAGCGAAAGAGAG	2059
Db	617	SerGlnGlnAlaThrIleLysTyrPyrIleGlnArgSerGlyAspGluHisArgGluGlu	636
QY	2060	ATCAGAGTGATGATCATATCATCATCAGACAGATCAAGGCGCTTCGTAGTGTCTACAA	2119
Db	637	LeuLysProAspGluArgIleIleLysThrGluTyrGlyLeuLeuIleArgSerLeuGln	656
QY	2120	CAGAAGATTCAGCAATACCTCTCCATGCGGTGGAAACATGGGTTCATACAACTCTT	2179
Db	657	LysLysAspSerGlyMetTyrTyrCysLysAlaGlnGluHisThrPheIleHisThrIle	676
QY	2180	CTTAAGGTAAACCTCGAAGTCATTGACACAGACATTTGGAAGAATCTTCTCATAAAGAT	2239
Db	677	ValLysLeuThrLeuAsnValIleGluAsnGluGlnMetGluAsnThrGlnArgAlaGlu	696
QY	2240	GATCATGTGAGATGGCTCTTAAGACCAAGAAATGTCCAATAGCATGACACTGCCAGAAG	2299
Db	697	HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg	710
QY	2300	GTCTGCTACAGACATTCATGAGCTCATCAACCCCACTCAACAGATGGATGAG	2359
Db	711	LeuArgTyrLysAspTyrIleGlnIleLeuSerProAsnPhe---SerLeuAspGln	729
QY	2360	TTCGTGAAACAAGTTTGGAAAAGGACCGAAAACAACGTCGCCAAGGCCAGACATACC	2419
Db	730	TyrCysGluGlnMetTyrHisArgGluLysArgGlnArgAsnLysGlyGly-----	747
QY	2420	CGAGGGAACAGTAACAATGGAGACATTCAGAAGAAATAGAAGGTAGAAACAGGAGG	2479
Db	748	-----ProLysTyrLysHisMetGlnGluMetLysLysLysArgAsnArgArg	763
QY	2480	ACCCAC---GAATTTGAGAGGCGCCCGAGGTGTC	2512
Db	764	HisHisArgAspLeuAspGluLeuProArgAlaVal	775
RESULT 9			
US-10-201-858-348			
; Sequence 348, Application US/10201858			
; Publication No. US20040038337A1			
; GENERAL INFORMATION:			
; APPLICANT: Baker, Kevin P.			
; APPLICANT: Chen, Jian			
; APPLICANT: Desnoyers, Luc			
; APPLICANT: Goddard, Audrey			
; APPLICANT: Godowski, Paul J.			
; APPLICANT: Gurney, Austin L.			
; APPLICANT: Pan, James			
; APPLICANT: Smith, Victoria			
; APPLICANT: Watanabe, Colin K.			
; APPLICANT: Wood, William I.			
; APPLICANT: Zhang, Zemin			
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC			

DECLASSIFIED

US-10-201-858-348
; Sequence 348, Application US/10201858
; Publication No. US20040038337A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRADE

QY	863	AA	TGATCCAAAGATTCATTAGTGCCACCTCATCTCAGAGAGTGAACAATCTCTGAAGATGAC	922
DB	239	AS	NGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAsp	258
QY	923	AA	AGATATACCTTTTCTCCGTGAAATGCAATAGATGGAGAACACTCTCTGGAAAAGCTACT	982
DB	259	LY	SIIeTyPhePhePheArgGluSerGlnGluGlySerThrSerAspLysThrIle	278
QY	983	CA	CGCTAGAATAGCTCAGATATGCAAGATGACTTTGGAGGGCAACAAGTCTCGTGAAT	1042
DB	279	LE	uSerA-gValGlyA-gValCysLysAsnAspValGlyGlnArgSerLeuIleAsn	298
QY	1043	AA	ATCGCAACAACATCTCCAAAGCTCGTCTGATTGTCTCAGTCCAGAGTCCAAATGGCATT	1102
DB	299	LY	STToThrPheLeuLysAlaA-gLeuIleCysSerIleProGlySerAspGlyAla	318
QY	1103	GA	CACTCAATTTTGATGAATCGCAGGATGTATTCCTAATGAACCTTTAAAGAACTCTTAA	1162
DB	319	AS	PTyPheAspGluLeuGlnAspIleTyrLeuLeuProThrArgAspGluArgAsn	338
QY	1163	CA	CGTTGATATGAGAGTGTTCACGACTCCAGTAAACATTTTCAAGGGATCAGCCGTGTGT	1222
DB	339	PR	oValValTyrGlyValPheThrThrThrSerSerIlePheLysGlySerAlaValCys	358
QY	1223	AT	GTATACATGATGATGTGAGAGGGTGTCTTGTCCATATGCCACAGGGATGGA	1282
DB	359	VA	lTySerMetAlaAspIleA-gAlaValPheAsnGlyProTyrAlaHisLeuGluSer	378
QY	1283	CC	CAACTATCAATGGGTCCCTTATCAAGGAAGTCCCTTATCCAGCCGACGAACTTGT	1342
DB	379	Al	AspHisA-gTTPValGlnTyrAspGlyArgIleProTyrProArgProGlyThrCys	398
QY	1343	CC	CAACAACATTTGGTGGT---TTTGACTCTACAAAGACCTTCCTGATGATCTATA	1399
DB	399	PR	oSerLysThrTyrAspProLeuIleLysSerThrArgAspPheProAspAspValIle	418
QY	1400	AC	CTTTGCAAGAAGTCATCCAGGCATGTACAATCCAGTGTTCCTATGAACAATCGCCCA	1459
DB	419	SE	rPheIleLysArgHisSerValMetTyrLysSerValTyrProValaGlyGlyPro	438
QY	1460	AT	AGTATCAAAACCGATGAAATTTCAATTTTACAAATTTGCTAGACCGAGTGGAT	1519
DB	439	TH	rPheLysArgIleAsnValAspTyrArgLeuThrGlnIleValValAspHisValIle	458
QY	1520	GC	AGAAGTACGACAGTATGATGTATTTATCCGAACAGAGTGTGGACCGCTCTTAAA	1579
DB	459	Al	aGluAspGlyGlnTyrAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys	478
QY	1580	GT	AGTTTCAATTCCTAAGGAGACTTGCTATGATTAGAGAGGTTCCTCGTGGAAAGATG	1639
DB	479	VA	ValSerIleSerLysGluLysTrp---AsnMetGluGluValValLeuGluGluLeu	497
QY	1640	AC	AGTTTTCGGAACCGACTGTATTTACGCAATGGAGCTTTCCTAAGCAGACACAA	1699
DB	498	GL	nIlePheLysHisSerSerIleLeuLeuAsnMetGluLeuSerLeuLysGlnGln	517
QY	1700	CT	ATATATTTGGTTCAAAGCGTGGGGTTCGCCAGCTCCCTTTACCCGGTGTGATTATTC	1759
DB	518	LE	uTyIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTyr	537
QY	1760	GG	AAAGCGTGTGCTAGTGTCCCTCGCCGAGACCTTACTGTGCTTGGGATGGTTCT	1819
DB	538	GL	YLysAlaCysAlaAspCysLeuLeuA-gAspProTyrCysAlaTrpAspGlyAsn	557
QY	1820	GC	ATTTCTCGTATTTTCCCACTGCACAAGACGCAACAAGACGACATATAAGAAAT	1879
DB	558	Al	aCysSerA-gTyrAlaProThrSerLysArgA-gAlaA-gArgGlnAspValLysTyr	577
QY	1880	GG	AGACCACCTGACTCTACTGTTCAGACTTACACATGATAATCACCATGGCCACAGCCCT	1939
DB	578	GL	AspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla	596

1940 GAAGAGAGAAATCATCTATGTGTGTAGAGATAGTAGACAAATTTTGGAAATGCAGTCCGAG 1999
 597 AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys 616
 2000 TCGCAGAGAGCGCTGGTCTTATGGCAATTCACAGAGCGGAAATGAAGACGAAAGAAAGAG 2059
 617 SerGlnGlnAlaThrIleLysTrpTyrIleGlnArgSerGlyAspGluHisArgGluGlu 636
 2060 ATCAGATGGATGATCATATCATCAGACAGACAGATCAAGGCTTCCTACGTACTGTACAA 2119
 637 LeuLysProAspGluArgIleLysThrGluTyrGlyLeuLeuIleArgSerLeuGln 656
 2120 CAGAAGGATTACGCAATTAACCTCTCCCATCGGTGGAAACATGGGTTTCATCAAACTCTT 2179
 657 LysLysAspSerGlyMetTyrTyrCysLysAlaGlnGluHisThrPheIleHisThrIle 676
 2180 CTTTAGGTAAACCTCGAAGTCATTGACACAGACGATTTGGAGAACTTCTTCATAAAGAT 2239
 677 ValLysLeuThrLeuAsnValIleGluAsnGluGlnMetGluAsnThrGlnArgAlaGlu 696
 2240 GATGATGAGATGCTCTTAAGACAAAGAAATGTCCAATAGCATGACACCTAGCAGAG 2299
 697 HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg 710
 2300 GTCCTGTACAGACTTCATCGAGCTCATCAACACCCCAATCTCAACACGATGGATGAG 2359
 711 LeuArgTyrLysAspTyrIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln 729
 2360 TTCTGTGAACAAAGTTTGGAAAAAGGACCGAAACAACTGTCGCGAAAGCCAGGACATACC 2419
 730 TyrCysGluGlnMetTrpHisArgGluLysArgGlnArgAsnLysGlyGly----- 747
 2420 CCAGGGAACACTAACTGGAAGCACTTACAGAGAAATTAAGAAAGGTAGAAACAGGAGG 2479
 748 -----ProLysTrpLysHisMetGlnGluMetLysLysLysArgAsnArgArg 763
 2480 ACCGAC---GAATTGAGCGGACCCAGGAGTGTC 2512
 764 HisHisArgAspLeuAspGluLeuProArgAlaVal 775
 RESULT 11
 US-10-208-024-348
 ; Sequence 348, Application US/10208024
 ; Publication No. US20040048335A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3430R1C538
 ; CURRENT APPLICATION NUMBER: US/10/208,024
 ; CURRENT FILING DATE: 2002-07-29
 ; PRIOR APPLICATION NUMBER: 10/052566
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-16
 ; PRIOR APPLICATION NUMBER: 60/059266
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063120
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063121
 ; PRIOR FILING DATE: 1997-10-24

; PRIOR APPLICATION NUMBER: 60/063486
 ; PRIOR FILING DATE: 1997-10-21
 ; PRIOR APPLICATION NUMBER: 60/063540
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063541
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063544
 ; PRIOR FILING DATE: 1997-10-28
 ; Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 348
 ; LENGTH: 777
 ; TYPE: PRT
 ; ORGANISM: Homo Sapien
 ; US-10-208-024-348

Alignment Scores:

Pred. No.: 1-9e-201 Length: 777
 Score: 2245.50 Matches: 413
 Percent Similarity: 73.67% Conservative: 141
 Best Local Similarity: 54.92% Mismatches: 177
 Query Match: 21 Indels: 21
 DB: 12 Gaps: 9

US-09-774-490-1 (1-2709) x US-10-208-024-348 (1-777)

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QY 275 AAGAACTGTCGAAGCTGAAATTCCTTACAAAGAAATGTTGGATCCAACTATG 334
Db 39 LysGlnAsnIleProArgLeuLysLeuThrTyrLysAspLeuLeuSerAsnSerCys 58
QY 335 ATCACTTTCAATGGCTGGCCACAGCTCCAGTATCATCACTTCCTTTTGGATGAGAA 394
Db 59 IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuLeuAspGlu 78
QY 395 CGGAGTAGCTGTATCTGGAGCAAGGATCATATTTTCATTCAGCTGTTAATATC 454
Db 79 ArgGlyArgLeuLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu 98
QY 455 ---AAGATTTCAAAGATTGTTGGCCAGTATCTTACACAGAGAGATCAATGCAAG 511
Db 99 AsnLysAspPheLysIleTyrTrpProAlaLysGluArgValGluLeuCysLys 118
QY 512 TGGCTGGAAAGACATCTGAAAGAAATGCTAATTCATCAAGGTACTTAAGGCATAT 571
Db 119 LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPheIleArgValLeuGlnProTyr 138
QY 572 ATCACTGCTATGTTACCTGTGGACGGGGCTTTTCATCAATTCACCTACAT 631
Db 139 AsnLysThrHisIleTyrValCysGlyThrGlyAlaPheHisProIleCysGlyTyrIle 158
QY 632 GAAATGGACATCATCTCGAGCAACAATATTTTAAGCTGGAGAACTCATATTTGAAAC 691
Db 159 AspLeuGlyValTyrLysGluAspIleIlePheLysLeuAspThrHisAsnLeuGluSer 178
QY 692 GCGGTGGGAAGAGTCCATATGACCTAGCTGCTGACAGACATCCCTTTTAATAGATGA 751
Db 179 GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu 198
QY 752 GAATATATCTCGGAATCTGACGTGATTTTATGGGCGAGACTTTGCTATCTCCGACT 811
Db 199 TyrLeuTyrSerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218
QY 812 CTGGG-----CACACACCAATCAGGACAGACAGCATGATTCAGGTGGCTC 862
Db 219 LeuGlyProThrHisAspHisIleTyrIleArgThrAspIleSerGluHisTyrTrpLeu 238
QY 863 ATGATCCAAAGCTTCATAGTCCACCTCATCTCAGAGATGACAAATCCTGAAGATGAC 922
Db 239 AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyrAsnProAspAsp 258
QY 923 AAAGTATATCTTTTCTCGTGAAATGATAGATGAGAACTCTGGGAAAGACTACT 982
Db 259 LysIleTyrPhePheArgGluSerGlnGluGlySerThrSerAspLysThrIle 278

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QY 983 CACGCTAGATAGTGCATATGCAAGATGACTTTGGAGGCGACAGAGCTGCTGGTGAAT 1042
Db 279 LeuSerArgValGlyArgValCysLysAsnAspValGlyGlyGlnArgSerLeuIleAsn 298
QY 1043 AAATGGACAACATTCCTCAAGCTCGTCTGATTTTCTCAGTGCCAGGTCCTCAATGGCAT 1102
Db 299 LysTrpThrThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla 318
QY 1103 GACACTCATTTTGTAGTACGAGATGCTATTCATGAACCTTAAAGATCCTCAAAAT 1162
Db 319 AspThrTyrPheAspGluLeuGlnAspIleTyrLeuLeuProThrArgAspGluArgAsn 338
QY 1163 CCAGTTGTATATGGAGTGTTTTACGACTTCCAGTAACATTTTCAAGGATCAGCCGTGTGT 1222
Db 339 ProValValTyrGlyValPheThrThrSerSerIlePheLysGlySerAlaValCys 358
QY 1223 ATGTATAGCATGATGATGAGAGGGTGTTCCTGGTCCATATGCCCACAGGATGGA 1282
Db 359 ValTyrSerMetAlaAspIleArgAlaValPheAsnGlyProTyrAlaHisLysGluSer 378
QY 1283 CCCAATCATCAATGGTGCCTTATCAAGGAAGAGTCCCTTATCCAGCGCCAGGAACCTTGT 1342
Db 379 AlaAspHisArgTrpValGlnTyrAspGlyArgIleProTyrProArgProGlyThrCys 398
QY 1343 CCCAGCAAAACATTTTGTGTGT---TTGACTCTCAAAAGGACCTTCTCTGATGATGTTATA 1399
Db 399 ProSerLysThrTyrAspProLeuIleLysSerThrArgAspPheProAspAspValIle 418
QY 1400 ACCTTTCCAGAAAGTCATCCAGCCATGATCAATCCAGTGTTCCTATGAACAATCGGCCA 1459
Db 419 SerPheLysArgHisSerValMetCysLysSerValTyrProValAlaGlyGlyPro 438
QY 1460 ATAGTGTCAAAACCGATGTAATTCATCAATTTACACAAATTTGTCGAGACCGAGTGGAT 1519
Db 439 ThrPheLysArgIleAsnValAspTyrArgLeuThrGlnIleValValAspHisValIle 458
QY 1520 GCAGAGATCGACATGATGATGTTATGTTATCGGAACAGATGTTGGACCGTCTTAA 1579
Db 459 AlaGluAspGlyGlnTyrAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys 478
QY 1580 GTAGTTTCAATTCCTAAGGAGACTGTTGATGATTTAGAGAGGTTCTGCTGGAGAAATG 1639
Db 479 ValValSerIleSerLysGluLysTrp---AsnMetGluValValLeuGluGluLeu 497
QY 1640 ACAGTTTTCGGAAACCGACTGCTATTTCAGCAATGAGGCTTCCACTAAGCAGCAACAA 1699
Db 498 GlnIlePheLysHisSerSerIleLeuAsnMetGluLeuSerLeuLysGlnGln 517
QY 1700 CTATATATTGTTCAACGGCTGGGTTGCCAGCTCCCTTTACACCGGTGTGATATTAC 1759
Db 518 LeuTyrIleGlySerArgAspGlyLeuValGlnLeuSerLeuHisArgCysAspThrTyr 537
QY 1760 GGAAGACGCTGCTGAGTGTTCCTCGCCGAGACCTTACTGTGCTGGGATGTTCT 1819
Db 538 GlyLysAlaCysAlaAspCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlyAsn 557
QY 1820 GCATGTTCTCGCTATTTTCCACTGCAAGAGACGCGACAGAGCAGACAGATATAAGAAAT 1879
Db 558 AlaCysSerArgTyrAlaProThrSerLysArgAlaArgArgGlnAspValLysTyr 577
QY 1880 GGAGACCACTGACTGCTTCCAGACTTACCATGATAATCACCATGATGATGATGATGAT 1939
Db 578 GlyAspProIleThrGlnCysTrpAspIleGluAspSerIleSerHis---GluThrAla 596
QY 1940 GAAGAGAGATCATCTATGTTGTAGAGATAGTAGACATTTTGGAAATGCACTGCTCGAAG 1999
Db 597 AspGluLysValIlePheGlyIleGluPheAsnSerThrPheLeuGluCysIleProLys 616
QY 2000 TCCAGAGAGCGCTGCTTATTCGCAATTCAGAGCGGAAATGAAGAGCGGAAAGAGAG 2059
Db 617 SerGlnGlnAlaThrIleLysTrpTyrIleGlnArgSerGlyAspGluHisArgGluGlu 636

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; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 348
; LENGTH: 777
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-201-853-348

Alignment Scores:
Pred."No.:      1.9e-201      Length:          777
Score:          2245.50       Matches:         413
Percent Similarity: 73.67%    Conservative:     141
Best Local Similarity: 54.92%  Mismatches:      177
Query Match:      45.86%     Indels:           21
DB:               12        Gaps:             9

US-09-774-490-1 (1-2709) x US-10-201-853-348 (1-777)

QY   275 AAGAACATGTGCCAAGCTGAATAATTCTACAAAGAATAATTGGATCCACAAATGTC 334
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   39 LysGlnAsnIleProArgLeuLysLeuThrTyLysAspLeuLeuSerAshSerCys 58
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   335 ATCACTTTCAATGCCTTGGCCAAAGCTCCAGTTATCATACCTTCCTTTTGATCAGGAA 394
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   59 IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuLeuAspGlu 78
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   395 CGGAGTAGCGTGTATGTGGCAAAGGATCACATATTTTCATTGCGACTGGTTAATATC 454
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   79 ArgGlyArgLeuLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu 98
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   455 ---AAGATTTTCAAAGATTGTGCGCCAGTATCTTACACCAGAGAGATGAATGCAAG 511
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   99 AsnLysAsnPhelLysLysIleTyTrProAlaAlaLysGluArgValGluLeuCysLys 118
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   512 TGGCGTGGAAAGACATCTCGAAAGATGTGCTAATTTTCATCAAGTACTTAAGGCATAT 571
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Db   119 LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPhelIleArgValLeuGlnProTyr 138
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QY   572 AATCAGACTCACTTGTACGCGCTGTGGAACGGGGCTTTTCATCCAATTTGCACCTACATT 631
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Db   139 AsnLysThrHisIleTyValCysGlyThrGlyAlaPheHisProileCysGlyTyFile 158
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QY   632 GAATTTGACATCATCTCTGAGGACATATTTTAACTGCGAGAACTCAATTTGAAAAC 691
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   159 AspLeuGlyValTyLysGluAspIleIlePheLysLeuAspThrHisAsnLeuGluSer 178
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   692 GGCGGTGGGAGAGTCCATATGACCTTACCTTACAGCTGCTGACAGCATCCCTTTTAAATAGATGGA 751
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Db   179 GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu 198
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QY   752 GAATTTACTCTGGAAGTCCAGCTGATTTTATGGGCGAGACTTTGCTATCTTCGGAAT 811
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Db   199 TyrLeutySerGlyThrAlaSerAppPheLeuGlyLysAspThrAlaPheThrArgSer 218
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QY   812 CTTGG3-----CACCACCAACCAATCAGACAGACAGCATGATTCACAGTGGCTC 862
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Db   219 LeuGlyProThrHisAspHisHisTyIleArgThrAspIleSerGluHisTyTripleu 238
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QY   863 AATGATCCAAAGTTCATTAGTGGCCACCTCATCTCAGAGAGTGACAATCCCTCAGATGAC 922
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   239 AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyAsnProAspAsp 258
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QY   923 AAAGTATACTTTTTCTTCCTGAAAAATGCAATAGATGGAGAACACATCTTGGAAAAGCTACT 982
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   259 LysIleTyPhePhePheArgGluSerSerGlnGlySerThrSerAspLysThreFile 278
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   983 CACGCTGAATAGTTCAGATATCAAGATGACTTTGGAGGGCACAGAAAGTCTGTTGAAT 1042
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db   279 LeuSerArgValGlyArgValCysLysAsnAspValGlyGlnArgSerLeuIleasn 298
    ||| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY   1043 AAATGGACACATTCCTCAAAGCTCTGCTGATTTGCTCMGTGCCAGGTCCAAATGGCATT 1102
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Db   299 LysTrpThrThrPheLeuLysAlaArgLeuIleCysSerIleProGlyLysSeraspGlyala 318
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1 PRIOR APPLICATION NUMBER: 60/065311
2 PRIOR FILING DATE: 1997-11-13
3 PRIOR APPLICATION NUMBER: 60/066120
4 PRIOR FILING DATE: 1997-11-21
5 PRIOR APPLICATION NUMBER: 60/066466
6 PRIOR FILING DATE: 1997-11-24
7 PRIOR APPLICATION NUMBER: 60/066772
8 PRIOR FILING DATE: 1997-11-24
9 PRIOR APPLICATION NUMBER: 60/069335
10 PRIOR FILING DATE: 1997-12-11
11 PRIOR APPLICATION NUMBER: 60/069425
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13 PRIOR APPLICATION NUMBER: 60/069870
14 PRIOR FILING DATE: 1997-12-17
15 PRIOR APPLICATION NUMBER: 60/068017
16 PRIOR FILING DATE: 1997-12-18
17 PRIOR APPLICATION NUMBER: 60/077450
18 PRIOR FILING DATE: 1998-03-10
19 PRIOR APPLICATION NUMBER: 60/077632
20 PRIOR FILING DATE: 1998-03-11
21 PRIOR APPLICATION NUMBER: 60/077649
22 PRIOR FILING DATE: 1998-03-11
23 PRIOR APPLICATION NUMBER: 60/078886
24 PRIOR FILING DATE: 1998-03-20
25 PRIOR APPLICATION NUMBER: 60/078939
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27 PRIOR APPLICATION NUMBER: 60/079664
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34 PRIOR FILING DATE: 1998-03-31
35 PRIOR APPLICATION NUMBER: 60/080327
36 PRIOR FILING DATE: 1998-04-01
37 PRIOR APPLICATION NUMBER: 60/080333
38 PRIOR FILING DATE: 1998-04-01
39 PRIOR APPLICATION NUMBER: 60/081049
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50 PRIOR FILING DATE: 1998-04-21
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52 PRIOR FILING DATE: 1998-04-22
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56 PRIOR FILING DATE: 1998-04-28
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63 PRIOR APPLICATION NUMBER: 60/083559
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65 PRIOR APPLICATION NUMBER: 60/084366
66 PRIOR FILING DATE: 1998-05-05
67 PRIOR APPLICATION NUMBER: 60/084414
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70 PRIOR FILING DATE: 1998-05-07
71 PRIOR APPLICATION NUMBER: 60/084640
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; PRIOR APPLICATION NUMBER: 60/089514
 ; PRIOR FILING DATE: 1998-06-16
 ; PRIOR APPLICATION NUMBER: 60/089538
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089598
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089653

Alignment Scores:

Pred. No.: 1,9e-201 Length: 777
 Score: 2245.50 Matches: 413
 Percent Similarity: 73.67% Conservative: 141
 Best Local Similarity: 54.92% Mismatches: 177
 Query Match: 45.86% Indels: 21
 DB: 12 Gaps: 9

US-09-774-490-1 (1-2709) x US-10-174-581-348 (1-777)

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 Db 39 LysGlnAsnIleProArgLeuLysLeuThrTyLysAspLeuLeuSerAsnSerCys 58
 QY 335 ATCACTTTCAATGGCTGGCCACAGCTCCAGTTATCATACCTTCCTTTGGATGAGAA 394
 Db 59 IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuLeuAspGlu 78
 QY 395 CGAGTAGCTGTATGTTGAGCAAGGATCATATTTTCATTCGACCTGGTTAATATC 454
 Db 79 ArgGlyArgLeuLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu 98
 QY 455 ---AAGGATTTCAAAGATTGTTGGCCAGTATCTTACACAGAGAGATGAATGCGAAG 511
 Db 99 AsnLysAsnPheLysIleTyTrpProAlaAlaLysGluArgValGluLeuCysLys 118
 QY 512 TGGCTGGAAAAGACATCTGAAAGAAATGCTTAATTCATCAAGTACTTAAGCATAT 571
 Db 119 LeuAlaGlyLysAspAlaAsnThrGluCysAlaAsnPheIleArgValLeuGlnProTy 138
 QY 572 ATCAAGACTACTGTACGCTGTGAAACGGGGCTTTTCATCCAAATTTGACCTACAT 631
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 QY 632 GAAATGGACATCATCTCAGGACAAATATTTTAAAGCTGGAGAACTCATATTTTAAAC 691
 Db 159 AspLeuGlyValTyLysGluAspIleIlePheLysLeuAspThrHisAsnLeuGluSer 178
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 Db 179 GlyArgLeuLysCysProPheAspProGlnGlnProPheAlaSerValMetThrAspGlu 198
 QY 752 GAATTATCTCGGAAGTCACTGATGATTTTATGGGGCGAGACTTTGCTATCTCCGAAC 811
 Db 199 TyrLeuTySerGlyThrAlaSerAspPheLeuGlyLysAspThrAlaPheThrArgSer 218
 QY 812 CTTGGG-----CACCAACACCAATCAGACAGACAGCATGATCCAGGTGGCTC 862
 Db 219 LeuGlyProThrHisAspHisIleTyTrpIleArgThrAspIleSerGluHisTyTrpLeu 238
 QY 863 AATGATCCAAAGTTCAATTAGTCCCACTCTCTCAGAGAGTGAACAATCTCGAAGATGAC 922
 Db 239 AsnGlyAlaLysPheIleGlyThrPhePheIleProAspThrTyLysAsnProAspAsp 258
 QY 923 AAAGTATATCTTTCTTCGTTGCAATGCAATGATGAGACACTCTGGAAAGACTACT 982
 Db 259 LysIleTyPhePhePheArgGluSerGlnGluGlySerThrSerAspLysThrIle 278
 QY 983 CACGTAGAAATAGGTGAGATATGCAAGATGACTTTTGGAGGGCACAGAGTCTGGTGAAT 1042
 Db 279 LeuSerArgValCylArgValCysLysAsnAspValGlyGlyGlnArgSerLeuIleAsn 298
 QY 1043 AAATGACAACTTCTCAAGCTCTGCTGATTCTCAGTCCAGGTCGAAATGGCAT 1102
 Db 299 LysTrpThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla 318

QY 1103 GACACTCATTTTGTATGAATGAACTGAGATGATTCCTTAATGAATCTTAAAGATCTTAA 1162
 Db 319 AspThrTyPheAspGluLeuGlnAspIleTyLysLeuLeuProThrArgAspGluArgAsn 338
 QY 1163 CCAGTTGTATATGAGTGTATACGACTTCCAGTACCAATTTTCAAGGGATCCAGCTGTGT 1222
 Db 339 ProValValTyGlyValPheThrThrSerSerIlePheLysGlySerAlaValCys 358
 QY 1223 ATGTATAGCATGAGTGTGAGAGGGTGTTCCTTGTGTCATATGCCACAGGATGGA 1282
 Db 359 ValTySerMetAlaAspIleArgAlaValPheAsnGlyProTyAlaHisLysGluSer 378
 QY 1283 CCCAACTATCAATGGTCCCTTATCAAGAAAGATCCCTATCCAGCCGACAGGAACTTGT 1342
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 Db 399 ProSerLysThrTyAspProLeuIleLysSerThrArgAspPheProAspAspValle 418
 QY 1400 ACCTTTGCAAGAAGTATCCAGCCATGATCAATCCAGTGTTCCTATGAAACAATCGGCCA 1459
 Db 419 SerPheIleLysArgHisSerValMetTyLysSerValTyProValAlaGlyGlyPro 438
 QY 1460 ATAGTATCAAAAACGAGTGAATTAATTTACAAATTTACAAATTTGCTAGACCGAGTGGAT 1519
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 QY 1520 GCAGAGATGACAGTATGATGTTATGTTATCGAAACAGATGTTGGACCGTCTTCTTAAA 1579
 Db 459 AlaGluAspGlyGlnTyAspValMetPheLeuGlyThrAspIleGlyThrValLeuLys 478
 QY 1580 GTAGTTCAATTCCTAAGGACATGTTGATGATTTTACAGAGGTTCTGCTGGAAGATG 1639
 Db 479 ValValSerIleSerLysGluLysTrp---AsnMetGluGluValValLeuGluGluLeu 497
 QY 1640 ACAGTTTTCGGGAACCGAGTGTATTTTCAGCAATGAGCTTTCCACTAAGCAGCAACAA 1699
 Db 498 GlnIlePheLysHisSerSerIleIleLeuAsnMetGluLeuSerLeuLysGlnGln 517
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 QY 2120 CAGAAGATTACAGCAATTTACTCTCTGCGATGCGGTGGAACATGGGTTCATACAACTCT 2179
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QY 1520 GCAGAGATGAGCAGTATGATGTTATGTTTATCGAACAAGATGTTGGACCTCTTAA 1579
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QY 1580 GTAGTTTCAATCCCTAAGAGACTGCTGATGATGTTAAGAGAGTCTGCTGGAAGAATG 1639
Db 479 ValValSerIleSerLysGluLysTrp---AsnMetGluGluValValLeuGluGluLeu 497
QY 1640 ACAATTTTTCGGAAACCGACTGCTATTTTCAGCAATGGAGCTTTCCACTAAGCAGCAACA 1699
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QY 1760 GGAAGAGCTGCTGAGTGGTTCCTCGCCCGAGACCTTACTGCTGCTGGATGCTTCT 1819
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QY 1880 GGAGACCCACTGACTGCTGCTGCTACACTTACACCATGATATCACCATGGCCACAGCCCT 1939
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QY 2000 TGCAGAGAGCGCTGCTATTGGCAATTCAGAGCGGCAAAATGAAGAGCGAAAGAGAG 2059
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QY 2060 ATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTACTACAA 2119
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QY 2180 CTTAAGGTAAACCTGGAAGTCTATGACAGAGCATTTGGAGAAGCTTCTTCATAAAGAT 2239
Db 677 ValLysLeuThrLeuAsnValIleGluAsnGluGlnMetGluAsnThrGlnArgAlaGlu 696
QY 2240 GATGATGGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATCACACCTAGCCAGAG 2299
Db 697 HisGluGluGlyGlnValLys-----AspLeuLeuAlaGluSerArg 710
QY 2300 GTCTGTGACAGACTTCATGAGCTCATCAACACCCCAATCTCAACACGATGATGAG 2359
Db 711 LeuArgTyLysAspTyIleGlnIleLeuSerSerProAsnPhe---SerLeuAspGln 729
QY 2360 TTCTGTGAACAAGTTTGGAAAGGACCGAACAACGCTCGCAAGGCGGACGACATACC 2419
Db 730 TyrCysGluGlnMetTrpHisArgGluLysArgGlnArgGlnArgGlnGlyGly----- 747
QY 2420 CCAGGGAACAGTAACAATGGAAGCACTTACAGAAATAAGAAAGGTAGAAACAGGAGG 2479
Db 748 -----ProLysTrpLysHisMetGlnGluMetLysLysLysArgAsnArgArg 763
QY 2480 ACCAC---GAATTCAGAGGCGCACCCAGGAGTCTC 2512
Db 764 HisHisArgAspLeuAspGluLeuProArgAlaVal 775
```

RESULT 15

US-10-176-749-348

; Sequence 348, Application US/10176749

; Publication No. US20030017542A1

; GENERAL INFORMATION:

```
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C76
; CURRENT APPLICATION NUMBER: US/10/176,749
; CURRENT FILING DATE: 2002-06-20
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 348
; LENGTH: 777
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-176-749-348
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Alignment Scores:

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Best Local Similarity: 54.92% Mismatches: 177
Query Match: 45.86% Indels: 21
DB: 12 Gaps: 9
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US-09-774-490-1 (1-2709) x US-10-176-749-348 (1-777)

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QY 335 ATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATACCTTCCTTTTGGATGAGAA 394
Db 59 IleProPheLeuGlySerSerGluGlyLeuAspPheGlnThrLeuLeuAspGluGlu 78
QY 395 CGAGTAGGCTGATGTTGGAGCAAGGATCACAATTTTCATCGACCTGGTTAATATC 454
Db 79 ArgGlyArgLeuLeuLeuGlyAlaLysAspHisIlePheLeuLeuSerLeuValAspLeu 98
QY 455 ---AAGATTTCCTCAAGATTTGTGTGCCAGTATCTTACACCAAGAGAGATGAATGCAAG 511
Db 99 AsnLysAsnPheLysLysIleTyTrpProAlaLysGluArgValGluLeuCysLys 118
QY 512 TGGCTGGAAGAACATCCTCGAAGATGTGCTAATTTTCATCAAGTACTTAAGGCATAT 571
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Db 159 AspLeuGlyValTyLysGluAspIleIlePheLysLeuAspThrHisAsnLeuGluSer 178
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Db 279 LeuSerArgValGlyArgValCysLysAsnAspValGlyGlyIleAsnSerLeuIleAsn 298
QY 1043 AAATGGACAATCTCTCAAGCTCGTCTGATTGCTCAGTCCAGGTCCTCAAAATGGCAAT 1102
Db 299 LysTrpThrThrPheLeuLysAlaArgLeuIleCysSerIleProGlySerAspGlyAla 318
QY 1103 GACACTCATTTGATGACTGAGGATGATTCCTTAATCAACTTTAAAGATCCTAAAT 1162
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QY 2240 GATGATGGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGCACACCTAGCCAGAAG 2299
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Job time : 398 secs

GenCore version 5.1.6
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OM nucleic - protein search, using frame_plus_n2p model

Run on: September 21, 2004, 19:36:33 ; Search time 53.5 Seconds
(without alignments)
5229.215 Million cell updates/sec

Title: US-09-774-490-1

Perfect score: 4896

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Ygapop 10.0 , Ygapext 0.5
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Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 778928

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	4201	85.8	771	1	US-08-835-268-54
3	4201	85.8	771	2	US-09-060-692-54
4	4201	85.8	771	3	US-08-833-391-54
5	4201	85.8	771	4	US-09-060-610-54
6	4201	85.8	771	5	PCT-US94-10151A-54
7	3568	72.9	655	4	US-08-556-422A-3
8	2562	52.3	477	1	US-08-136-922-2
9	2030	41.5	775	4	US-09-308-179B-1
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11	838.5	17.1	607	4	US-08-556-422A-4
12	817	16.7	1070	4	US-09-653-274-8

13	817	16.7	1086	4	US-09-653-274-4	Sequence 4, Appli
14	816.5	16.7	641	4	US-09-653-274-13	Sequence 13, Appl
15	785.5	16.0	724	1	US-08-121-713D-62	Sequence 62, Appl
16	785.5	16.0	724	1	US-08-835-268-62	Sequence 62, Appl
17	785.5	16.0	724	2	US-09-060-692-62	Sequence 62, Appl
18	785.5	16.0	724	3	US-08-833-391-62	Sequence 62, Appl
19	785.5	16.0	724	4	US-09-060-610-62	Sequence 62, Appl
20	785.5	16.0	724	5	PCT-US94-10151A-62	Sequence 62, Appl
21	785.5	15.6	536	4	US-09-653-274-10	Sequence 10, Appl
22	765.5	15.6	930	4	US-09-254-594-6	Sequence 6, Appl
23	762.5	15.6	730	1	US-08-121-713D-58	Sequence 58, Appl
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25	762.5	15.6	730	2	US-09-060-692-58	Sequence 58, Appl
26	762.5	15.6	730	3	US-08-833-391-58	Sequence 58, Appl
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31	738.5	15.1	650	2	US-09-060-692-60	Sequence 60, Appl
32	738.5	15.1	650	3	US-08-833-391-60	Sequence 60, Appl
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34	738.5	15.1	650	5	PCT-US94-10151A-60	Sequence 60, Appl
35	723.5	14.8	929	4	US-09-254-594-3	Sequence 3, Appl
36	723	14.8	887	4	US-09-077-940A-2	Sequence 2, Appl
37	718	14.7	425	4	US-08-556-422A-7	Sequence 7, Appl
38	712.5	14.6	888	4	US-09-077-940A-4	Sequence 4, Appl
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40	680	13.9	712	1	US-08-835-268-64	Sequence 64, Appl
41	680	13.9	712	2	US-09-060-692-64	Sequence 64, Appl
42	680	13.9	712	3	US-08-833-391-64	Sequence 64, Appl
43	680	13.9	712	4	US-09-060-610-64	Sequence 64, Appl
44	680	13.9	712	5	PCT-US94-10151A-64	Sequence 64, Appl
45	654.5	13.4	666	3	US-09-240-410-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-121-713D-54
; Sequence 54, Application US/08121713D
; Patent No. 5639856
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthews, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713D
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36, 627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:

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; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-121-713D-54

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Alignment Scores:		
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DB:	1	0
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Matches:		771
Conservative:		0
Mismatches:		0
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US-09-774-490-1 (1-2709) x US-08-121-713D-54 (1-771)

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21	AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu	40
320	GAATCCAACAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATACCTTC	379
41	GlusSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerSerTyrHisThrPhe	60
380	CTTTTGGATGAGGAACCGAGTAGGCTGTATGTTGGAGCAAGAGATCACATATTTTCATTC	439
61	LeuLeuaspGluGluArgSerArgLeuTyrValGlyAlaLysAsnHisIlePheSerPhe	80
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81	AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg	100
500	GATGAATGCAAGTGGGCTGGAAAGACATCCTCAAAAGAAATGTCTAAATTCATCAAGGTA	559
101	AspGluCysLysTTPalaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal	120
560	CTTAAGGCATATATACAGACTCATTGTAGCCCTGTGGAAACGGGGCGCTTTTCATCCAATT	619
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680	CATTTTGAACCGCCCTGGGAGAGAGTCCATATGACCTTAAGCTGCTGACAGCATCCCTT	739
161	HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu	180
740	TTAATAGATGAGAAATATACTCTGGAACCTGCAGCTGATTTTATGGGCGAGACTTGCT	799
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201	IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGlnHisAspSerArgTrp	220
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920	GACAAAGTATACTTTTCTTCCTGCGAAATGCAATAGATGGAGACACTCTTGGAAAAGCT	979
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RESULT 2
US-08-835-268-54
; Sequence 54, Application US/08835268
; Patent No. 5807826
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,268
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.80% Indels: 0
DB: 1 Gaps: 0

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QY 620 TGCACCTACATTGAAATGGACATCATCTGAGAGCAATATTTTAACTGGGAGAACTCA 679
Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTCAAAACGGCGTGGGAAGTCCATATGACCTTAAGCTGCTGACAGCATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGAGAATTATATCTCTGGAACCTGCAGCTGATTTTATGGGCGGAGACTTTGCT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCGAACTCTTGGGACACCCACCACCAATCAGACAGACAGCATGATTCAGGTGG 859
Db 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCATGATCCAAAGTTTCATTAGTGGCCACTCATCTCAGAGAGTGCATATCTGGAAGAT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATACCTTTTCTCCGTGAAATGCAATAGATGGAGAACACTCTGGAAGCT 979
Db 241 AspLysValTyrPhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ACTCAGCTAGATAGTTCAGATATCAAGAATGCTTTGGAGGGCACAGAGCTCTGGTG 1039
Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisArgSerLeuVal 280
QY 1040 AATAATGGACAACATTCCTCAAAGCTCGTCTGATTGCTAGTGGCAGGTCCAAATGGC 1099
Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
QY 1100 ATTGACACTCATTTTGTGATGACTGCAGGATGTATTCTTAATGAACTTAAAGATCTCTAAA 1159
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Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPhenylsAspProlys 320
 QY 1160 AATCAGTGTATATGAGGTGTTTACGACTTCAGTAACTTTCAGGATCAGCCGTG 1219
 Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLeuGlySerAlaVal 340
 QY 1220 TGTATGTATAGCATGAGTGTGAGAGGGTCTCTTGGTCCATATGCCACAGGAT 1279
 Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgasp 360
 QY 1280 GGACCCCAACTCAATCGGTCCTTATCAAGGAGAGTCCCTTCCAGGCCAGGAAC 1339
 Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
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 Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
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 Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
 QY 1520 GCAGAGATCGACAGTATGATGTATGTTTATCGGAACAGATGTTGGACCGTCTTAAA 1579
 Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
 QY 1580 GTAGTTCATTCCTAAGAGAGCTTGATGATGTTAGAGAGCTTCTGCTGGAAGAATG 1639
 Db 461 ValValSerIleProLysGlnThrTrpTyrAspLeuGluGluValLeuLeuGluMet 480
 QY 1640 ACAGTTCCTCGGAACCGACTGCTATTTCAGCAATGGAGCTTCCACTAAGCAGCAACA 1699
 Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
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 Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
 QY 1760 GGGAAACGGTCTGAGTGTTCCTCGCCGAGACCTTACTGTGCTGGATGGTCT 1819
 Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
 QY 1820 GCATGTCTCGCTATTTCCACTGCAAGAGACGCACAGACGACAGATATAGAAT 1879
 Db 541 AlaCysSerArgTyrPheProThrAlaLysArgA-gThrA-gArgGlnAspIleArgAsn 560
 QY 1880 GGAGACCACTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1939
 Db 561 GlyAspProLeuThrHisCysSerAspLeuHisH-asPAsnHisHisGlyHisSerPro 580
 QY 1940 GRAGAGATCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1999
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 Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnA-gA-gAsnGluGluArgLysGluGlu 620
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 Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
 QY 2120 CAGAGGATTCAGGCAATTTACTCTGCCATGCGGTGGAACATGGGTTCATCAAACTCT 2179
 Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
 QY 2180 CTTAAGTACCTGCACTGCTTACACAGAGCATTTGGAAGACTTCTCTAAAGAT 2239

Db 661 LeuLysValThrIleuGluValIleAspThrGluHisLeuGluLeuLeuHisLysAsp 680
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 Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
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 QY 2360 TTCTGTGAACAAGTTTGAAAAAGGACCCGAAACAAACATCGCGAAAGCCAGGACATACC 2419
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 QY 2480 ACCACGAATTTGAGAGGCGACCCAGGAGTCTC 2512
 Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771
 RESULT 3
 US-09-060-692-54
 ; Sequence 54, Application US/09060692
 ; Patent No. 5935865
 ; GENERAL INFORMATION:
 ; APPLICANT: Goodman, Corey S.
 ; APPLICANT: Kolodkin, Alex L.
 ; APPLICANT: Mattes, David
 ; APPLICANT: Bentley, David R.
 ; APPLICANT: O'Connor, Timothy
 ; TITLE OF INVENTION: The Semaphorin Gene Family
 ; NUMBER OF SEQUENCES: 100
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 Bush Street, Suite 3200
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/09/060,692
 ; FILING DATE:
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/121,713
 ; FILING DATE: 13-SEP-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Osman, Richard A.
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: B94-002-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415) 343-4341
 ; TELEFAX: (415) 343-4342
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 54:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 771 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-09-060-692-54
 Alignment Scores:
 Pred. No.: 0
 Score: 4201.00
 Percent Similarity: 100.00%
 Length: 771
 Matches: 771
 Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.80% Indels: 0
DB: 2 Gaps: 0

US-09-774-490-1 (1-2709) x US-09-060-692-54 (1-771)

QY 200 ATCGGCTGGTAACTAGGATGCTCTCTTCTGGGAGTATTACTTACAGCAGAGCA 259
Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuThrAlaArgAla 20
QY 260 AACTATCAGAAATGGGAAGAACAAATGTGCCAAGGCTCAAAATATCTCTACAAAGAAATGTG 319
Db 21 AsnTyrgluAsnGlyLysAsnValProArgLeuLysLeuSerTyrlsGluMetLeu 40
QY 320 GAATCCAAATGTGATCACTTTCAATGGCTTGGCCAAACAGCTCCAGTTTATCATACCTTC 379
Db 41 GluSerAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrlsHisThrPhe 60
QY 380 CTTTTCGATCAGGAACGGAGTAGCTGTATGTGGAGCAAGGATCACATATTTTCATTC 439
Db 61 LeuLeuAspGluArgSerArgLeuTyrlsValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGGTTAATATCAAGGATTTTCAAAAGATTGTGGCCCAAGTATCTTACACCAAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyrlsArgArg 100
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Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATTAATCAGACTCACTTGTACGGCTGTGGAAACGGGGCTTTTCATCCAATT 619
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QY 620 TGCACCTCATGAAATTCGACATCATCTGAGGACAAATATTTTAAAGCTGAGAACTCA 679
Db 141 CysThrTyrlsIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTGAACCGCGCTGGAGAGTCCATATGACCTAAGCTGCTGACACATCCCTT 739
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QY 740 TTAATAGATGGAATATATCTCTGGAATCTGAGCTGATTTTATGGGCGAGACTTCT 799
Db 181 LeuIleAspGlyGluLeuTyrlsSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCGAACTTGGCACCACCACTCAATCAGGACAGCAGCATGATTCAGGTGG 859
Db 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCATATGATCCAAAGTTTCAATAGTCCCACTCATCTCAGAGAGTGACAATCCTCAAGAT 919
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QY 920 GACAAAGTATCTTTTCTCGTGAATGCAATAGATGGAGACACTCTCGAAAGCT 979
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QY 980 ACTCAGCTAGAAATAGTATATGCAAGATGACTTTGGAGGGCAGCAAGAGTCTGGTG 1039
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QY 1100 ATTGACATCATTTTCACTGAGGATGATTTCTTCAATCAATCAATTTTAAAGATCCTTAA 1159
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QY 1160 AATCCAGTTCTATATCGAGTGTATTCAGACTTCAGATTAACATTTTCAAGGGATCACCGGT 1219
Db 321 AsnProValValTyrlsGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340

QY 1220 TGTATGTATAGCATGATGTGAGAAGGGTGTCTCTTGTGTCATATGCCACAGGAT 1279
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QY 1280 GGACCCAACTATCAATGGTGCCTTATCAAGGAAGAGTCCCTTATCCACGCCAGGAACT 1339
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QY 1340 TGTCCCAAGCAAAACATTTTGGTGGTTTCACTCTACAAAGGACCTTCTCTGATGATGTATA 1399
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QY 1400 ACCTTTGCAAGAAGTCTCCAGCCATGTACATCCAGTGTCTTCTATGAACAATCGGCCA 1459
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QY 1700 CTATATATTTGTTCAACGGCTGGGTTGCCAGCTCCCTTTACACCGTGTGATATTAC 1759
Db 501 LeuTyrlsIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyrls 520
QY 1760 GGGAAAGCTGTCTGAGTGTGCTCGCCGAGACCTTACTGTCTGTGGATGGTCT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrlsAlaTrpAspGlySer 540
QY 1820 GCATGTTCTGCTATTTTCCACCTGCAAGAGAGCGCAAGAGCAAGATATAAGAAAT 1879
Db 541 AlaCysSerArgTyrlsPheProThrAlaLysArgArgThrArgArgGlnAspIleArgAsn 560
QY 1880 GGACACCCACTGACTCACTGTTCAGACTTACACCATGATAATCACCATGCCACAGCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro 580
QY 1940 GAAGAGAGAATCATCTATGTTGATAGAGATAGTAGCACATTTTGGAAATGCAGTCCGAAG 1999
Db 581 GluGluArgIleIleTyrlsGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
QY 2000 TCGCAGAGAGGCTGGTCTATTGGCAATTCAGAGCGGAATGAGAGCGCAAGAGAGAG 2059
Db 601 SerGlnArgAlaLeuValTyrlsTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620
QY 2060 ATCAGAGTGAATGATCATATCATCAGACAGATCAAGCGCTTCTGCTACCTAGTCTACAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
QY 2120 CAGAAGGATTCAGCAATTAACCTCTGCTGCGGTGGAAACATGGGTTTCATCAAACTCTT 2179
Db 641 GlnLysAspSerGlyAsnTyrlsLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
QY 2180 CTTAAGGTAAACCTGGGAAGTCATTGACACAGAGCATTTGGAAGAACTTCTTCATAAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
QY 2240 GATGATGAGATGCTCTAAAGACAAAGAAATGTCCAATAGCATGACACCTGACCGAGAAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700

Thu Sep 23 08:54:06 2004

QY 2300 GTCTGGTACAGAGCTTCATCAGCTCATCAACACCCCAATCTCAACAGATGGATGAG 2359
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 QY 2420 CCAGGAACAGTAACAATGGAAGCAGCTTCAAGAAATAGAAAGTGAAGGAGG 2479
 Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysGlyArgAsnArgArg 760
 QY 2480 ACCACGAATTTGAGAGGCGCCAGGAGTGTCT 2512
 Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771

RESULT 4
 US-08-833-391-54
 ; Sequence 54, Application US/08833391
 ; Patent No. 6013781
 ; GENERAL INFORMATION:
 ; APPLICANT: Goodman, Corey S.
 ; APPLICANT: Kolodkin, Alex L.
 ; APPLICANT: Matthes, David
 ; APPLICANT: Bentley, David R.
 ; APPLICANT: O'Connor, Timothy
 ; NUMBER OF INVENTORS: The Semaphorin Gene Family
 ; NUMBER OF SEQUENCES: 100
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
 ; STREET: 268 Bush Street, Suite 3200
 ; CITY: San Francisco
 ; STATE: CA
 ; COUNTRY: USA
 ; ZIP: 94104
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/833,391
 ; FILING DATE:
 ; CLASSIFICATION: 530
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/121,713
 ; FILING DATE: 13-SEP-1993
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Osman, Richard A.
 ; REGISTRATION NUMBER: 36,627
 ; REFERENCE/DOCKET NUMBER: B94-002-1
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (415)343-4341
 ; TELEFAX: (415) 343-4342
 ; TELEX:
 ; INFORMATION FOR SEQ ID NO: 54:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 771 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 ; US-08-833-391-54

Alignment Scores:
 Pred. No.: 0
 Score: 4201.00
 Percent Similarity: 100.00%
 Best Local Similarity: 100.00%
 Query Match: 85.80%
 DB: 3
 Length: 771
 Matches: 771
 Conservative: 0
 Mismatches: 0
 Indels: 0
 Gaps: 0

US-09-774-490-1 (1-2709) x US-08-833-391-54 (1-771)

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 QY 260 AACTATCATGAGTGGAAAGCAAAATGTGCAAGGCTGAAATATTCTTACAAAGAAATGTTG 319
 Db 21 AsnTrpGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTrpLysGluMetLeu 40
 QY 320 GAATCAACAATGTGATCACTTTCAATGGCTGGCCAAACAGCTCCAGTTATCATCTTC 379
 Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerSerTrpHisThrPhe 60
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 Db 61 LeuLeuAspGluGluArgSerArgLeuTrpValGlyAlaLysAspHisIlePheSerPhe 80
 QY 440 GACCTGGTTATATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACACCAAGA 499
 Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTrpThrArgArg 100
 QY 500 GATGAATGCAAGTGGCTGGAAAGACATCTGGAAGATGCTGTAATTTTCATCAAGGTA 559
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 QY 620 TGCACCTACATTAATGGAATGGAATCTGAGGACATATTTTAAAGCTGGAGAACTCA 679
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 QY 680 CATTGTGAAGCGGCGCTGGAGAGTCCATATGACCTCAAGCTGTCAGACATCCCTTT 739
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 QY 1160 AATCCAGTTGTATATGAGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1219
 Db 321 AsnProValValTrpGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
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QY 1340 TGCCAGCAAAACATTTGGTGGTTGGTCTCTACAAAGACCTTCCTGATGATGTATA 1399
Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspValIle 400
QY 1400 ACCTTTGCCAAGAGTCATCCAGCCATGTACAATCCAGTCTTTCCATGAACAATCGCCA 1459
Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
QY 1460 ATAGTGATCAAAACGAGTGAATATCAATTTACACAAATTTGCTAGACCGAGTGGAT 1519
Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
QY 1520 GCAGAAGATGGACAGATGATGTATGTTTTCGGAACAGATCTTGGGACCGCTTTTAAA 1579
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QY 1580 GTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAAAGAGTTCTGCTGAAAGAAATG 1639
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QY 1640 ACAGTTTTCGGGAACCGACTGCTATTTCCAGCAATGGAGCTTCCACTAAGCAGCAAA 1699
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QY 1820 GCATGTTCTCGCTATTTTCCCTGCAAGAGACGCAAGAGCAGCAAGATATAAGAAT 1879
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgThrArgArgGlnAspIleArgAsn 560
QY 1880 GGAGACCCACTGACTCAGTGTTCAGACTTACACCATGATAATCACCATGGCCACAGCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisGlyHisSerPro 580
QY 1940 GAAGAGAGATCATCTATGTTAGAGATAGTAGACACATTTTGGATGCGAGTCCGAG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
QY 2000 TCCGACAGAGCCGTCTATTGGCAATTCAGAGCGCAATGAAGAGCGAAAGAAAGAGAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgAsnGluGluArgLysGluGlu 620
QY 2060 ATCAGAGTGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTACGTAGTCTCAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
QY 2120 CAGAGAGTTACAGCAATTTACCTGCGCATGGTGGGACATGGGTTTCATCAAACTCTT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
QY 2180 CTTAAGGTAAACCTCGAAGTCTATTGACACAGACGATTTTGGAGAACTTCTTCATAAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuHisLysAsp 680
QY 2240 GATGATGGAGATGGCTCTAAGCAACCAAGAAATGTCATAGCATGACACCTAGCCAGAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
QY 2300 GTCTGGTACAGAGACTTCATGAGCTTCATCAACACCCCAATCTCAACACCATGATGAG 2359
Db 701 ValTrpTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
QY 2360 TTCTGTGAACAAGTTTGGAAAGGAGCCGAAACAAACGTCGGCAAGCCCGAGCATACC 2419

Db 721 PheCysGluGlnValTrpLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
QY 2420 CCAGGGAACAGTAAACAATGGAACACTTACAGAAAATAAGAAAGGTAGAAAACAGGAGG 2479
Db 741 ProGlyAsnSerAsnLysTrpLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760
QY 2480 ACCACCAATTTGAGAGCGCACCCAGGAGTGTCT 2512
Db 761 ThrHisGluPheGluArgAlaProArgSerVal 771
RESULT 5
US-09-060-610-54
; Sequence 54, Application US/09060610
; Patent No. 6344544
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthews, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/060,610
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/835,268
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 54:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 771 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-060-610-54
Alignment Scores:
Pred. No.: 0 Length: 771
Score: 4201.00 Matches: 771
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 85.80% Indels: 0
DB: 4 Gaps: 0
US-09-774-490-1 (1-2709) x US-09-060-610-54 (1-771)
QY 200 ATGGGCTGGTTAACTAGGATTGTCTGTTTCTGGGAGTATTACTTACAGCAAGACA 259
Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
QY 260 AACTATCAGAAATCGGAGAACAAATGTCCCAAGCTGAAATATCTTACAAAGAAATGTTG 319

Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GATCCAAACATGTGATCACTTTCAATGGCTGGCCCAACAGCTCCAGTTTATCATACCTTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyrHisThrPhe 60
QY 380 CTTTGGATGAGAACGGATAGCTGTATGTGGAGCAAGATGACATATTTTCATTC 439
Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
QY 440 GACCTGTTTAAATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACACCAAGA 499
Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValIleThrProValSerTyrThrArg 100
QY 500 GATGAATGCAAGTGGCTGGAAAGACATCTCTGAAGAAGATGTGCTAAATTTCAATCA 559
Db 101 AspGluCysIleThrAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATATCAAGACTCACTGTAGCTGTGGCAACGGGGCTTTTCATCCAATT 619
Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACTTACATGAATTTGACATCATCTCTGAGGACAAATATTTTAAAGCTGGAGAACTCA 679
Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTTTCGAACCGCTGGAGAGCTCCATATGACCTAAGCTCTGACAGCATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuThrAlaSerLeu 180
QY 740 TTAATAGATGAGAATTATCTCGAAGCTGAGCTGATTTTATGGGCGAGACTTTCCT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTCCGAAGCTCTGGGACACCAACCAATCAGACAGACAGCAGCATGATTCAGAGTGG 859
Db 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgIle 220
QY 860 CTCGAATGCAAGTTCATTTAGTCCCACTCATCTCAGAGATGACAACTCTGAAGAT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAATGATCTTTCTTCGTGAATGCAATGATAGATGGAGACACTCTGGAAAGCT 979
Db 241 AspLysValIlePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
QY 980 ACTCAGCTAGATAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1039
Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyHisArgSerLeuVal 280
QY 1040 AATAAATGGAACAATCTCTCAAGCTCTGCTGATTTGCTCAGTCCAGGTCCTCAATGGC 1099
Db 281 AsnLysThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
QY 1100 ATTGACACTCATTTGATGAAGTGCAGGATGATTTCTTAATGAATTTAAAGATCTTAA 1159
Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
QY 1160 AATCCAGTGTATAGAGTGTATAGCTTCCAGTCCAGTATCATTTTCAAGGATCAGCGTG 1219
Db 321 AsnProValValIleGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
QY 1220 TGTATGATAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1279
Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360
QY 1280 GGAACCAACTCATCAAGTGGCTTATCAAGAGAGTCCCTATCCACGCGCAGGAACT 1339
Db 361 GlyProAsnTyrGlnIleThrValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
QY 1340 TGTCACGACAAACATTTGGTGGTGTGTGATCTTCAAAAGGACCTTCTGATGATGATGAT 1399
Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspValIle 400

QY 1400 ACCTTTGCAAGAGTCACTCCAGCATGTACAACTCCAGTGTTCCTATGAACAATCGCCCA 1459
Db 401 ThrPheAlaIleArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
QY 1460 ATAGTATCAAAACCGATGTAAATTTATCAATTTACAAATTTGCTGAGACCGATGAT 1519
Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
QY 1520 GCAGAAGATGACACAGTATGATGATTTTTCGGAACAGATGTGGGACCGTTCCTTAAA 1579
Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
QY 1580 GTAGTTTCATTTCCCTAAGGAGACTTGTATGATTTAGAGAGGTTCTGCTGGAAGAATG 1639
Db 461 ValValSerIleProLysGluThrTrpTyrAspLeuGluValLeuLeuGluMet 480
QY 1640 ACAGTTTTCGGGAACCGACTGCTATTTTCAGCAATGAGCTTTCCACTAAGCAGCAACAA 1699
Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
QY 1700 CTATATATTGTTTCAACGGCTGGGTTGCCAGCTCCCTTTACACCGGTGTATTTAC 1759
Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
QY 1760 GGGAAAGCTGTGCTGAGTGTGCTCCCGCAGACCTTACTGCTTGGGATGGTTCT 1819
Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaIleAspGlySer 540
QY 1820 GCATGTTCTCGCTATTTTCCCACTGCAAGAGACGCAAGACGACAGATATTAAGAAAT 1879
Db 541 AlaCysSerArgTyrPheProThrAlaLysArgArgThrArgGlnAspIleArgAsn 560
QY 1880 GGAGACCACTGACATCACTGTTTCAGACTTACACCATGATATACCATGCGCCACAGCCCT 1939
Db 561 GlyAspProLeuThrHisCysSerAspLeuHisAspAsnHisHisGlyHisSerPro 580
QY 1940 GAAGAGAGATCATCTTATGTTGAGATAGTAGACATTTTGGGAATGAGTCCGAG 1999
Db 581 GluGluArgIleIleTyrGlyValGluAsnSerThrPheLeuGluCysSerProLys 600
QY 2000 TCGCAGAGAGCTGCTGCTATTGGCAATTCAGAGGCGAAATGAAGACGCAAGAAAGAG 2059
Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgAsnGluGluArgLysGluGlu 620
QY 2060 ATCAGAGTGGATGATCATCATGAGACAGATCAAGCCCTTCTGCTACGTAGCTACAA 2119
Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
QY 2120 CAGAAGGATTCAGGCAATTTACTCTGCTCCATCGGTGGAACATGGGTTTCATCAAACTCTT 2179
Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGlyPheIleGlnThrLeu 660
QY 2180 CTTAAGGTAACCTCGAAGTCAATTCACAGAGATTTTGGAGAACTTCTTCATTAAGAT 2239
Db 661 LeuLysValThrLeuGluValIleAspThrGluHisLeuGluGluLeuLeuHisLysAsp 680
QY 2240 GATGATGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAGCCAGAAG 2299
Db 681 AspAspGlyAspGlySerLysThrLysGluMetSerAsnSerMetThrProSerGlnLys 700
QY 2300 GTCTGGTACAGAGACTTCATGACCTTCATCAACACCCCAATCTCAACAGATGATGAG 2359
Db 701 ValTyrTyrArgAspPheMetGlnLeuIleAsnHisProAsnLeuAsnThrMetAspGlu 720
QY 2360 TTCTGTGAACAAAGTTTGGAAAAGGACCGAAACAAAGCTCGCAAGAGCCGACGACATACC 2419
Db 721 PheCysGluGlnValTyrLysArgAspArgLysGlnArgGlnArgProGlyHisThr 740
QY 2420 CCAGGAAACAGTAACAAATGGAAGCCTTACAGAAATTAAGAAAGGTAGAAACAGGAGG 2479
Db 741 ProGlyAsnSerAsnLysThrLysHisLeuGlnGluAsnLysLysGlyArgAsnArgArg 760

QY 2480 ACCACGAATTCGAGGGCACCCAGAGTGC 2512
 Db 761 ThrHisGluPheGluAraGalaProArgSerVal 771

RESULT 6

PCT-US94-10151A-54
 ; Sequence 54, Application PC/TUS9410151A
 ; GENERAL INFORMATION:
 ; APPLICANT: The Regents of the University of California
 ; TITLE OF INVENTION: The Semaphorin Gene Family
 ; NUMBER OF SEQUENCES: 66
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: FLEHR HOCHBACH TEST ALBRITTON & HERBERT
 ; STREET: 4 Embarcadero Center, Suite 3400
 ; CITY: San Francisco
 ; STATE: CA

COUNTRY: USA
 ZIP: 94111-4187
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: PCT/US94/10151A
 FILING DATE: 13-SEP-1994
 CLASSIFICATION:
 ATTORNEY/AGENT INFORMATION:

NAME: Osman, Richard A.
 REGISTRATION NUMBER: 36,627
 REFERENCE/DOCKET NUMBER: FP-58750-PC/RAO
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (415) 781-1989
 TELEFAX: (415) 398-3249
 TELEX: 910 277299 FHT UR
 INFORMATION FOR SEQ ID NO: 54:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 771 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 PCT-US94-10151A-54

Alignment Scores:

Pred. No.: 0 Length: 771
 Score: 4201.00 Matches: 771
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 85.80% Indels: 0
 DB: 5 Gaps: 0

US-09-774-490-1 (1-2709) x PCT-US94-10151A-54 (1-771)

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 Db 21 AsnTyrGlnAsnGlyLysAsnValProArgLeuLysLeuSerTyLysGluMetLeu 40
 QY 320 GAATCCAAATGTGATCACTTTCATGCTGGCCACAGCTCCAGTTATCATACCTTC 379
 Db 41 GluSerAsnValIleThrPheAsnGlyLeuAlaAsnSerSerTyHisThrPhe 60
 QY 380 CTTTGGATGAGGAACGGAGTAGGCTGTATGTGGAGCAAGGATCACATATTTTCATTC 439
 Db 61 LeuLeuAspGluArgSerArgLeuTyrValGlyAlaLysAspHisIlePheSerPhe 80
 QY 440 GACCTGGTTAATCAAGATTTTCAAAGATTGTGCGCCAGTATCTTACACGAGAAGA 499
 Db 81 AspLeuValAsnIleLysAspPheGlnLysIleValTrpProValSerTyThrArg 100

QY 500 GATGAATGCAAGTGGCTGGAAAAGACATCTCTGAAAAGATGTGTAATTTCAATCAAGTA 559
 Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
 QY 560 CTTAAGGCATATAATCAGACTCACTGTAGCCCTGTGGAACGGGGCTTTTTCATCCAATT 619
 Db 121 LeuLysAlaTyrAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
 QY 620 TGCACCTACATTTGAAATTTGGACATCATCTGAGGACAAATATTTTAAAGCTGGAGAATCA 679
 Db 141 CysThrTyrIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
 QY 680 CATTTTGAACCGCGCTGGGAGAGTCCATATCACCTAAGCTGCTGACAGCATCCCTT 739
 Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
 QY 740 TTAATAGATGGAGAAATTATATCTCTGGAATCGACCTGATTTTATGGGGCGAGACTTTGCT 799
 Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
 QY 800 ATCTTCGAACTCTTGGGCACCCACCACCAATCAGGACAGACAGCATGATTCAGGTGG 859
 Db 201 IlePheArgThrLeuGlyHisHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
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 QY 920 GACAAAGTATACCTTTTCTCCGTGAAAATGCAATAGATCGAGAACACTCTGGAAGACT 979
 Db 241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260
 QY 980 ACTCACGCTAGATAGTTCAGATATGCAAGAATGACTTTGAGGGGACAGAGTCTGGTG 1039
 Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyGlyHisAspSerLeuVal 280
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 Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuIleCysSerValProGlyProAsnGly 300
 QY 1100 ATTGACACTCATTTTGATGAACCTGCAGGATGTTATCTTAATGAACCTTAAAGATCCTAAA 1159
 Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
 QY 1160 AATCCAGTGTATATGGAGTGTATTACGACTTCAGTAAACATTTTCAAGGATCAGCGGTG 1219
 Db 321 AsnProValValTyrGlyValPheThrThrSerSerAsnIlePheLysGlySerAlaVal 340
 QY 1220 TGTATGTATAGCATGATGATGTGAGAAGGGTGTCTTGGTCCATATGCCACAGGAT 1279
 Db 341 CysMetTyrSerMetSerAspValArgValPheLeuGlyProTyrAlaHisArgAsp 360
 QY 1280 GGACCCCAACTATCAATGGGTGCCTTATCAAGGAAGAGTCCCTTATCCAGCGCCAGGAAC 1339
 Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
 QY 1340 TGTCACAGCAAAACATTTGGTGGTTTTGACTCTACAAAGGACCTTCTGATGATGTATA 1399
 Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspAspValIle 400
 QY 1400 ACCTTTGCAAGAAGTCAATCCAGCCATGTACAAATCCAGTGTTCCTTATGAACAATCGCCA 1459
 Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnArgPro 420
 QY 1460 ATAGTGATCAAAACGGATGTAAATTTATCAATTTACACAAATTTCTGTAGACCCAGTGGAT 1519
 Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
 QY 1520 GCGAAGATCGACAGATGATGATGTTATTCGGAACAGATGTTGGGCCCTTCTTAA 1579
 Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
 QY 1580 GTAGTTTCAATTCTTAAGGAGACTTGGTATGATTTTAGAAGAGGTTCTGTGGAAGAAATG 1639

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; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DFN-005CPA2
; CURRENT APPLICATION NUMBER: US/08/556,422A
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 655
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-08-556-422A-3

Alignment Scores:
Pred. No.: 0 Length: 655
Score: 3568.00 Matches: 655
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 72.88% Indels: 0
DB: 4 Gaps: 0

US-09-774-490-1 (1-2709) x US-08-556-422A-3 (1-655)

QY 200 ATGGCTGCTTAACTAGGATTGCTCTCTTCTGGGAGTATTACTTACAGCAGAGCA 259
Db 1 MetGlyTrpLeuThrArgIleValCysLeuPheTrpGlyValLeuLeuThrAlaArgAla 20
QY 260 AACTATCAGAATGGGAAGCAAAATGTGCCAAGGCTGAAATATCTCTCAAGAAATCTTG 319
Db 21 AsnTyrGlnAsnGlyLysAsnAsnValProArgLeuLysLeuSerTyrLysGluMetLeu 40
QY 320 GAATCCACAATGTCATCACTTCAATGCTTCAATGCTTGGCCACAGCTCCAGTTCATACCTTC 379
Db 41 GluSerAsnAsnValIleThrPheAsnGlyLeuAlaAsnSerSerSerTyrHisThrPhe 60
QY 380 CTTTGGATGAGGAACGGAGTAGGCTGTATGCTTGGACCAAGGATCATATTTTTCATTC 439
Db 61 LeuLeuAspGluGluArgSerArgLeuTyrValGlyAlaLysAspHisPheSerPhe 80
QY 440 GACCTGGTAAATATCAAGATTTCAAAGATTGTTGGCCAGTATCTTACACAGAGCA 499
Db 81 AspLeuValAlaSerIleLysAspPheGlnLysIleValTrpProValSerTyrThrArgArg 100
QY 500 GATGAATCAAGTGGGCTGGAAAGACATCTCTGAAAGAAATGTCTAAATTTTCATCAAGGTA 559
Db 101 AspGluCysLysTrpAlaGlyLysAspIleLeuLysGluCysAlaAsnPheIleLysVal 120
QY 560 CTTAAGGCATATAATCAGACTCATTGTACGCTGTGACGGGGGCTTTTCATCCAAAT 619
Db 121 LeuLysAlaLysAsnGlnThrHisLeuTyrAlaCysGlyThrGlyAlaPheHisProIle 140
QY 620 TGCACCTCAATTTGAAATTTGGACATCATCTCGAGGACAATATTTTAAAGCTGGAGAACTCA 679
Db 141 CysThrTrpIleGluIleGlyHisHisProGluAspAsnIlePheLysLeuGluAsnSer 160
QY 680 CATTGTGAAAACGGCCGTGGGAAGATTCATATCCCTAAGCTGCTGACAGCATCCCTT 739
Db 161 HisPheGluAsnGlyArgGlyLysSerProTyrAspProLysLeuLeuThrAlaSerLeu 180
QY 740 TTAATAGATGGAAGATTATATCTTGGAACTGACCTGATTTTATGGGGCGAGACTTTGCT 799
Db 181 LeuIleAspGlyGluLeuTyrSerGlyThrAlaAlaAspPheMetGlyArgAspPheAla 200
QY 800 ATCTTCGNACTCTTGGCCACCAACCAATCAGGACAGGACAGCATGATCCAGGTGG 859
Db 201 IlePheArgThrLeuGlyHisHisProIleArgThrGluGlnHisAspSerArgTrp 220
QY 860 CTCAATGATCCAAAGTTTCATTAGTGGCCACCTCATCTCAGAGAGTGACAAATCTCGAGAT 919
Db 221 LeuAsnAspProLysPheIleSerAlaHisLeuIleSerGluSerAspAsnProGluAsp 240
QY 920 GACAAAGTATATCTTTCTTCCGTGAAATGTCATATGAGAACACTCTGGAAAGCT 979
Db 241 AspLysValTyrPhePhePheArgGluAsnAlaIleAspGlyGluHisSerGlyLysAla 260

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RESULT 7

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US-08-556-422A-3
; Sequence 3, Application US/08556422A
; Patent No. 6576754
; GENERAL INFORMATION:
; APPLICANT: HALL, Kathryn T.
; APPLICANT: FREEMAN, Gordon J.
; APPLICANT: SCHULTZE, Joachim I.
; APPLICANT: BOUSSIERIS, Vassiliki
; APPLICANT: NADLER, Lee M.

```

QY 980 ACTCAGCTAGATAGTACATATGCAAGAAATGACTTTGGAGGACACAGAAATCTGGTG 1039
 Db 261 ThrHisAlaArgIleGlyGlnIleCysLysAsnAspPheGlyHisArgSerLeuVal 280
 QY 1040 AATAATGACACATCTCTCAAGCTCGTCTGATTTGCTCAGTGCAGCGTCAATGGC 1099
 Db 281 AsnLysTrpThrThrPheLeuLysAlaArgLeuLeuCysSerValProGlyProAsnGly 300
 QY 1100 ATTGACACTCATTTTGCATGAACGTCAGGATGTATCTCAATGAACCTTTAAAGATCTTAA 1159
 Db 301 IleAspThrHisPheAspGluLeuGlnAspValPheLeuMetAsnPheLysAspProLys 320
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 Db 361 GlyProAsnTyrGlnTrpValProTyrGlnGlyArgValProTyrProArgProGlyThr 380
 QY 1340 TGTCCAGCAACAATTTGGTGGTGTGTGACTCTACAAAGACCTTCCTGATGATTTATA 1399
 Db 381 CysProSerLysThrPheGlyGlyPheAspSerThrLysAspLeuProAspValIle 400
 QY 1400 ACCTTTGCAAGAGTCAATCCAGCCATGTACATCCAGTGTTCCTATGAACAAATGCCCA 1459
 Db 401 ThrPheAlaArgSerHisProAlaMetTyrAsnProValPheProMetAsnAsnArgPro 420
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 Db 421 IleValIleLysThrAspValAsnTyrGlnPheThrGlnIleValValAspArgValAsp 440
 QY 1520 GCAGAAGATGCGACGATGATGTTATGTTTTCGGAACAGATGTTGGGACCGTCTCTTAA 1579
 Db 441 AlaGluAspGlyGlnTyrAspValMetPheIleGlyThrAspValGlyThrValLeuLys 460
 QY 1580 GTAGTTTCAATTCCTAAGGAGCTGGTATGATTTAGAGAGTTCCTGCTGGAAGAAATG 1639
 Db 461 ValValSerIleProLysGlnThrTrpTyrAspLeuGluValLeuLeuGluMet 480
 QY 1640 ACAGTTTTTCGGGAACCGACTCTATTTTCAGCAATGGAGCTTCCACTAAGCAGCAAA 1699
 Db 481 ThrValPheArgGluProThrAlaIleSerAlaMetGluLeuSerThrLysGlnGln 500
 QY 1700 CTATATATTGTTCAACGGCTGGGTTGCCAGCTCCCTTTACACCGGTGTGATATTTAC 1759
 Db 501 LeuTyrIleGlySerThrAlaGlyValAlaGlnLeuProLeuHisArgCysAspIleTyr 520
 QY 1760 GGAAGAGCTGTGAGTGTGCTCGCCGAGACCTTACTGTGCTGTGGAGTGTCT 1819
 Db 521 GlyLysAlaCysAlaGluCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlySer 540
 QY 1820 GCATGTTCTCGCTATTTTCCCACTGCAAGACGACCAAGACGACCAAGATATAGAAT 1879
 Db 541 AlaCysSerArgTyrPheProThrAlaLysArgThrArgArgGlnAspIleArgAsn 560
 QY 1880 GGAGACCCACTGACTCATGTTTCAGACTTACACCATGATATACCATGGCCACAGCCCT 1939
 Db 561 GlyAspProLeuThrHisCysSerAspLeuHisHisAspAsnHisHisGlyHisSerPro 580
 QY 1940 GAAGAGAGATCATCTATGTTGTAGAGATAGTACACATTTTGGATGAGTCCGAG 1999
 Db 581 GluGluArgIleIleTyrGlyValGluAsnSerSerThrPheLeuGluCysSerProLys 600
 QY 2000 TCCAGAGAGCGCTGCTCTATTGGCAATTCAGAGCGCAATGAAGAGCGAAAGAGAGAG 2059
 Db 601 SerGlnArgAlaLeuValTyrTrpGlnPheGlnArgArgAsnGluGluArgLysGluGlu 620

QY 2060 ATCAGAGTGGATGATCATATCATCATCAGGACAGATCAAGCCCTTCTGCTAGTACTCAA 2119
 Db 621 IleArgValAspAspHisIleIleArgThrAspGlnGlyLeuLeuLeuArgSerLeuGln 640
 QY 2120 CAGAAGATTCCAGCAATTAACCTCTGCGATCGGTGGAAACATGGG 2164
 Db 641 GlnLysAspSerGlyAsnTyrLeuCysHisAlaValGluHisGly 655

RESULT 8
 US-08-136-922-2
 ; Sequence 2, Application US/08136922
 ; Patent No. 5416197
 ; GENERAL INFORMATION:
 ; APPLICANT: Raper, Jonathan A.
 ; APPLICANT: Luo, Yuling
 ; TITLE OF INVENTION: Compositions Which Regulate Neural
 ; TITLE OF INVENTION: Regeneration and Methods of Making and Using the Same
 ; NUMBER OF SEQUENCES: 2
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
 ; ADDRESS: No. 5416197ris
 ; STREET: One Liberty Place
 ; CITY: Philadelphia
 ; STATE: PA
 ; COUNTRY: USA
 ; ZIP: 19103
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/136,922
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Deluca, Mark
 ; REGISTRATION NUMBER: 33,229
 ; REFERENCE/DOCKET NUMBER: UPN-1428
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 215-568-3100
 ; TELEFAX: 215-568-3439
 ; INFORMATION FOR SEQ ID NO: 2:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 477 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: protein
 US-08-136-922-2

Alignment Scores:
 Pred. No.: 2,31e-246 Length: 477
 Score: 2562.00 Matches: 472
 Percent Similarity: 99.37% Conservative: 0
 Best Local Similarity: 99.37% Mismatches: 3
 Query Match: 52.33% Indels: 0
 DB: 1 Gaps: 0

US-09-774-490-1 (1-2709) x US-08-136-922-2 (1-477)

QY 899 GAGAGTGACAATCTGAAGATGACAAAGTATATCTTTTCTCGTGAAATGCAATAGAT 958
 Db 2 GluHisAspAsnProGluAspAspLysValTyrPhePheArgGluAsnAlaIleAsp 21
 QY 959 GGAGAACACTCTGGAAGCTACTACCGTAGATAGGTAGATATGCAAGATGACATTT 1018
 Db 22 GlyGluHisSerGlyLysAlaThrHisAlaArgIleGlyGlnIleCysLysAsnAspPhe 41
 QY 1019 GGAGGGCACAGAGTCTGGTGAATAATGACAAACATTTCTCAAGCTCGTCTGATTTGC 1078
 Db 42 GlyGlyHisArgSerLeuValAsnLysTrpThrThrPheLeuLysAlaArgLeuIleCys 61
 QY 1079 TCAGTCCAGGTCCTCAAAATGGCATTTGACCTCATATTTTGTGATGAACTGAGGATGATTCCTA 1138

Db 62 SerValProGlyProAsnGlyIleAspThrHisPheAspGluLeuGlnAspValPheLeu 81
Qy 1139 ATGAACATTTAAAGATCCATAAATCCAGTTGTATATGGAGTGTGTACGACTTCCAGTAAC 1198
Db 82 MetAsnPheLysAspProLysAsnProValValValGlyValPheThrThrSerSerAsn 101
Qy 1199 ATTTTCAGGATCCAGCCGCTGTATGTATAGCATGAGTGTGAGAGGGTGTCCCTT 1258
Db 102 IlePheLysGlySerAlaValCysMetTyrSerMetSerAspValArgValPheLeu 121
Qy 1259 GGTCCATATGCCACAGGGATGACCCCACTATCAATGGTGCCTTATCAAGAAAGATC 1318
Db 122 GlyProTyrAlaHisAspGlyProAsnTyrGlnTyrValProTyrGlnGlyArgVal 141
Qy 1319 CCTATCCAGCCAGCAATCTCCACGCAAAACATTTGGTGTGTGACTCTCAAG 1378
Db 142 ProTyrProArgProGlyThrCysProSerLysThrPheGlyGlyPheAspSerThrLys 161
Qy 1379 GACCTTCTGATGTATTAACCTTTGCAAGAGATCATCCAGCCATGTACCAATCCAGTG 1438
Db 162 AspLeuProAspValIleThrPheAlaArgSerHisProAlaMetTyrAsnProVal 181
Qy 1439 TTTCTCTATGACAAATCCCAATAGTATCAACCGATGTAATATCAATTTACAAA 1498
Db 182 PheProMetAsnAsnArgProIleValIleLysThrAspValAsnTyrGlnPheThrGln 201
Qy 1499 ATTCTCTAGACCGAGTGGATGAGAGATGAGACATGATGTTATGTTATCGAACA 1558
Db 202 IleValValAspArgValAspAlaGluAspGlyGlnTyrAspValMetPheIleGlyThr 221
Qy 1559 GATCTTGGGACCGTCTTAACTACTTCAATTCCTAAGGAGACTTGTATGATTTAGAA 1618
Db 222 AspValGlyThrValLeuLysValValSerIleProLysGluThrTyrPyrAspLeuGlu 241
Qy 1619 GAGTTCTGTGGAAGAAATGACAGTTTTTCGGGAACCGACTGCTATTTACCAATGGAG 1678
Db 242 GluValLeuLeuGluGluMetThrValPheArgGluProThrAlaIleSerAlaMetGlu 261
Qy 1679 CTTTCCACTAAGCAGCAGCACTATATATGTTTCAACGGTGGGGTGGCCAGCTCCCT 1738
Db 262 LeuSerThrLysGlnGlnLeuLysIleGlySerThrAlaGlyValAlaGlnLeuPro 281
Qy 1739 TTACACCGGTGTGATATTTACGGGAAGCGTGTGCTGAGTGTGCTGCCCGAGACCT 1798
Db 282 LeuHisArgCysAspIleTyrGlyLysAlaCysAlaGluCysCysLeuAlaArgAspPro 301
Qy 1799 TACTGTCTTGGATGTTCTGCTGATCTTCTGCTATTTTCCACTGCCAAGAGACGACA 1858
Db 302 TyrCysAlaThrAspGlySerAlaCysSerArgTyrPheProThrAlaLysArgArgThr 321
Qy 1859 AGACGACAAGATATAAGAAATGGAGACCCACTGACTCTGCTACACTTACACCATGAT 1918
Db 322 ArgArgGlnAspIleArgAsnGlyAspProLeuThrHisCysSerAspLeuHisAsp 341
Qy 1919 AATCACCATGCCACACCGCTGAGAGAGAAATCATCTATGCTGTAGAGAAATGAGCACA 1978
Db 342 AsnHisHisGlyHisSerProGluGluArgIleIleTyrGlyValGluAsnSerThr 361
Qy 1979 TTTTGAATGCAATCCGAAAGTCGAGAGAGCGCTGTCTATTTGGCAATTCAGAGCGGA 2038
Db 362 PheLeuGluCysSerProLysSerGlnArgAlaLeuValTyrTrpGlnPheGlnArg 381
Qy 2039 AATCAAGAGCAAAAGAGATGACAGTGGATGATCATATCATCAGGACAGATCAAGC 2098
Db 382 AsnGluGluArgLysGluGluIleArgValAspAspHisIleIleIleArgThrAspGlnGly 401
Qy 2099 CTTCTGTACTAGTCTACAAACAGAGATTCAGGCAATTCCTCTGCACTCGGTGGAA 2158
Db 402 LeuLeuLeuArgSerLeuGlnLysAspSerGlyAsnTyrLeuCysHisAlaValGlu 421
Qy 2159 CATGGGTTCATCAAACTCTTCTTAAGGTAAACCTGGAAGTCAATTTGACACAGAGCATTTG 2218

Db 422 HisGlyPheIleGlnThrLeuLeuLysValThrLeuGluValIleAspAsnGluHisLeu 441
Qy 2219 GAAGAACTTCTTCAATAAAGATGATGATGAGATGCTCTTAAGACCAAGAAATGTCCAAT 2278
Db 442 GluGluLeuLeuHisLysAspAspGlyHisGlySerLysThrLysGluMetSerAsn 461
Qy 2279 AGCATCACACCTAGCACCAAGGTCTGTACAGAGACTTCATGCCAG 2323
Db 462 SerMetThrProSerGlnLysValTyrPyrArgAspPheMetGln 476
RESULT 9
US-09-308-1798-1
; Sequence 1, Application US/093081798
; Patent No. 6436669
; GENERAL INFORMATION:
; APPLICANT: FURUYAMA, Tatsuo
; TITLE OF INVENTION: NOVEL SEMAPHORIN GENES (I)
; FILE REFERENCE: 0020-4562P
; CURRENT APPLICATION NUMBER: US/09/308,1798
; CURRENT FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/JP97/04111
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: JAPAN 321068/1996
; PRIOR FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
; TYPE: PRT
; LENGTH: 775
; ORGANISM: Mus sp.
US-09-308-1798-1
Alignment Scores:
Pred. No.: 3,096-193 Length: 775
Score: 2030.00 Matches: 368
Percent Similarity: 67.75% Conservative: 155
Best Local Similarity: 47.67% Mismatches: 231
Query Match: 41.46% Indels: 18
Gaps: 8
DB: 4
US-09-774-490-1 (1-2709) x US-09-308-1798-1 (1-775)
Qy 218 ATGTCTGTCTTTCTGGGAGTATTACTTACAGCAAGCAAACTATCAGAATGGAG 277
Db 8 LeuThrLeuLeuLeuTrpGlyHisLeuLeuGluLeuTrpThrProGlyHisSerAlaAsn 27
Qy 278 AACATGTGCCAAGCTCAAAATTTCTACAAAGAAATGTTGGATCCAAATGTGATC 337
Db 28 ProSerTyrProArgLeuArgLeuSerHisLysGluLeuLeuGluLeuAsnArgThrSer 47
Qy 338 ACTTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATCTTCTCTTTTGGATGGAAACGG 397
Db 48 IlePheGlnSerProLeuGlyPheLeuAspLeuHisThrMetLeuLeuAspGluTyrGln 67
Qy 398 AGTAGCTGTATGTGGAGCAAGATGATCATATTTTCATTCGACCTGGTTAATATCAAG 457
Db 68 GluArgLeuPheValGlyArgAspLeuValTyrSerLeuLeuAsnLeuGluArgValSer 87
Qy 458 GAT---TTTCAAAGATGTTGTGGCCAGTATCTTTACACCAAGAGAGATGAATGCAAGTGG 514
Db 88 AspGlyTyrArgGluIleTyrTrpProSerThrAlaValLysValGluGluCysIleMet 107
Qy 515 GCTGGAAGACATCTGAAAGATGTGCTAATTTCTCAAGGTACTTAAGGCATATAAT 574
Db 108 LysGlyLysAsp---AlaAsnGluCysAlaAsnTyrIleArgValLeuHisHisTyrAsn 126
Qy 575 CAGACTCACTGTACCCCTGTGGAAACGGGGCTTTTTCATTCATTTGCACCTCATGTAA 634
Db 127 ArgThrHisLeuLeuThrCysAlaThrGlyAlaPheAspProHisCysAlaPheIleArg 146
Qy 635 ATTGGACATCATCTCTGAGGACAAATATTTTAAAGTGGAGAACTCACATTTTGAAGACGGC 694

Db 147 ValGlyHisSerGluGluProLeuPheHisLeuGluSerHisArgSerGluArgGly 166
QY 695 CGTGGAGAGTCCATATACCTAGCTGCTGACAGCATCCCTTTTATATAGATGGAGAA 754
Db 167 ArgGlyArgCysProPheAspProAsnSerSerPheValSerThrLeuValGlyAsnGlu 186
QY 755 TTATACCTCGGAACCTACGCTGATTTATGCGGCGAGACTTTCTCTATCTCCGAACTCTT 814
Db 187 LeuPheAlaGlyLeuTyrSerAspTyrTrpGlyArgAspSerAlaIlePheArgSerMet 206
QY 815 GGCACACACCCCAATCAGGACAGACAGCATGATTCAGAGTGGCTCAATGATCCAAAG 874
Db 207 GlyLeuGlyHisIleArgThrGluHisAspAspGluArgLeuLeuLysGluProLys 226
QY 875 TTCATTAGTGGCCACCTATCTCAGAGAGTGAACATCTGAGATGACAAAGTATCTTT 934
Db 227 PheValGlySerTyrMetIleProAspAsnGluAspArgAspAsnLysMetTyrPhe 246
QY 935 TTCTTCCTCGTGAATCAATAGATGAGAACACTCTGGAAAGACTACTCACCTAGAATA 994
Db 247 PhePheThrGluLysAlaLeuGluAlaGluAsnAsnAlaHisThrIleTyrThrArgVal 266
QY 995 GGTACAGATGACGAAGTACTTTGAGGGGCACAGAGTCTGGTGAATAAATGACACAA 1054
Db 267 GlyArgLeuCysValAsnAspMetGlyGlyGlnArgIleLeuValAsnLysTrpSerThr 286
QY 1055 TTCCTCAAGCTCGTCTGATTTGCTCAGTGGCCAGGTCCTCAAGTGGCATTGACACTATTT 1114
Db 287 PheLeuLysAlaArgLeuValCysSerValProGlyMetAsnGlyIleAspThrTyrPhe 306
QY 1115 GATGAACCTCAGGATGTATTCCTAATGAACCTTAAAGATCCTAAATCCAGTTGTATAT 1174
Db 307 AspGluLeuGluAspValPheLeuLeuProThrArgAspProLysAsnProValIlePhe 326
QY 1175 GGAGTGTTCACAGCTCCAGTACATTTTCAAGGATCAGCGTGTGTATGTATAGATG 1234
Db 327 GlyLeuPheAsnThrSerAsnIlePheArgGlyHisAlaValCysValTyrHisMet 346
QY 1235 AGTGTGTGAGAGGCTGTCTCTGTCATATGCCACAGGATGGACCCCACTATCAA 1294
Db 347 SerSerIleArgGluAlaPheAsnGlyProTyrAlaHisLysGluGlyProGluTyrHis 366
QY 1295 TGGTGCTTATCAGGAAGAGTCCCTATCCACGGCCAGAGAACTTGTCCGACGAAACA 1354
Db 367 TrpSerLeuTyrGluGlyLysValProTyrProArgProGlySerCysAlaSerLysVal 386
QY 1355 TTTGTGGT---TTTGACTCTCAAGAGACCTTCCTGATGATGTATTAACCTTTGCAAGA 1411
Db 387 AsnGlyGlyLysTyrGlyThrThrLysAspTyrProAspAspAlaIleArgPheAlaArg 406
QY 1412 AGTCATCCAGCCATGATACATCCAGTGTTCCTATGAACAATCGCCCAATAGTATCAAA 1471
Db 407 MetHisProLeuMetTyrGlnProIleLysProValHisLysLysProIleLeuValLys 426
QY 1472 ACGGATGTAAATATCAATTTACAAATTTGCTGATAGCCGAGTGGATGCGAGATGGA 1531
Db 427 ThrAspGlyLysTyrAsnLeuArgGlnLeuAlaValAspArgValGluAlaGluAspGly 446
QY 1532 CAGTATGATGTTATGTTATCGGAACACAGATGTGGGCGCTTCTTAAAGTAGTTCATTT 1591
Db 447 GlnTyrAspValLeuPheIleGlyThrAspThrGlyIleValLeuLysValIleThrIle 466
QY 1592 CTAAGGACACTGGTATGATTAAGAGGTTCTGCTGGGAAGAAATGACAGTGTTCGG 1651
Db 467 TyrAsnGlnGluThrGluTrpMetGluGluValIleLeuGluGluLeuGlnIlePheLys 486
QY 1652 GAACGACTGCTATTTCAGCAATGAGCTTTCCACTAAGCAGCAACAATATATATGCT 1711
Db 487 AspProAlaProIleSerMetGluIleSerSerLysArgGlnGlnLeuTyrIleGly 506
QY 1712 TCAACGCTGGGTTGCCAGCTCCCTTTACACCGGTGTGATATTACGGGAAAGCGGT 1771
Db 507 SerAlaSerAlaValAlaGlnValArgPheHisCysAspMetTyrGlySerAlaCys 526

QY 1772 GCTGAGTTGCTCCCTCGCCGAGACCTTACTGTCTTGGATGCTTCTGATGTTCTCGC 1831
Db 527 AlaAspCysCysLeuAlaArgAspProTyrCysAlaTrpAspGlyIleSerCysSerArg 546
QY 1832 TATTTTCCCACT-----GCAAGAGACGACACAGACACAGATATAAGAAATGGA 1882
Db 547 TyrTyrProThrGlyAlaHisAlaLysArgPheArgGlnAspValArgHisGly 566
QY 1883 GACCACCTGACTCTGTTCCAGACTTACACCATGATTAATCACCATGCGCCACAGCCCTGAA 1942
Db 567 AsnAlaAlaGlnGlnCysPheGlyGlnGlnPheValGlyAspAlaLeuAspArgThrGlu 586
QY 1943 GAGAGATCATCTATGCTGTAGAGATAGTAGACATTTTGGATCCAGCTCCGAATCG 2002
Db 587 GluArgLeuAlaTyrGlyIleGluSerAsnSerThrLeuLeuGluCysThrProArgSer 606
QY 2003 CAGAGAGCGTGTGCTATTGCAATTCAGAGCGGCAATGAAGAGCGCAAAAGAGAGATC 2062
Db 607 LeuGlnAlaLysValIleTyrPheValGlnLysGlyArgAspValArgLysGluGluVal 626
QY 2063 AGAGTGGATGATCATATCATCAGACAGATCAAGGCCTTCTGTACTGTACTTACACAG 2122
Db 627 LysThrAspAspArgValValLysMetAspLeuGlyLeuLeuPheLeuArgValArgLys 646
QY 2123 AAGGATTGAGCAATTAACCTCTGCTGCGTGGACATCGGTTCTACACAACTCTTCTT 2182
Db 647 SerAspAlaGlyThrTyrPheCysGlnThrValGluHisAsnPheValHisThrValArg 666
QY 2183 AAGTAAACCTGGAGTCTATTGACACAGACATTTGGAAGAACTTCTTATAAGATGAT 2242
Db 667 LysIleThrLeuGluValValGluGluHisLysValGluGlyMetPheHisLysAspHis 686
QY 2243 GATGGAGATGGCTCTAGACCAAGAAATGTCC-----AATACATGACACCT 2290
Db 687 GluGluGlu-----ArgHisLysMetProCysProProLeuSerGlyMetSerGln 704
QY 2291 AGCCAGAGGCTGTGGTACAGAGACTTCATCAGCTCATCAACACCCCAATCTCAACACG 2350
Db 705 GlyThrLysProTyrTyrLysGluPheLeuGlnLeuIleGlyTyrSerAsnPheGlnArg 724
QY 2351 ATGATGAGTCTGTGAAAGAGTTTGGAAAGGAGCGCAAAACACGCTCGGCAAGGCCA 2410
Db 725 ValGluGluTyrCysGluLysValTyrCysThrAspLysLysArgLysLysLeuLysMet 744
QY 2411 GGACATACCCCGAGGACAGTAAACAATGCAACACTTACAGAAAATAAGAAAGGTAGA 2470
Db 745 -----SerProSerLysTyrLysTyrAlaAsnProGlnGluLys---Arg 758
QY 2471 AACAGGAGGACCCAGCAATTTGAGAGGCGCACCCAGG 2506
Db 759 LeuArgSerLysAlaGluHisPheArgLeuProArg 770

RESULT 10

US-08-556-422A-2
; Sequence 2, Application US/08556422A
; Patent No. 6576754
; GENERAL INFORMATION:
; APPLICANT: HALL, Kathryn T.
; APPLICANT: FREEMAN, Gordon J.
; APPLICANT: SCHULTZE, Joachim L.
; APPLICANT: BOUSSETIOTIS, Vassiliki
; APPLICANT: NADLER, Lee M.
; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
; FILE REFERENCE: DFN-005CPA2
; CURRENT APPLICATION NUMBER: US/08/556,422A
; CURRENT FILING DATE: 1995-11-09
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 862
; TYPE: PRT
; ORGANISM: Homo sapiens

Db 623 GlnCysLeuSerGluGluArgValLysAsnLysThrValPheGlnValValAlaLysHis 642
 QY 2189 -----ACCTGGAAGTCATTGAC 2206
 Db 643 ValLeuGluValLysValValProLysProValValAlaProThrLeuSerValValGln 662
 QY 2207 ACAGAG 2212
 Db 663 ThrGlu 664

RESULT 11

US-08-556-422A-4
 ; Sequence 4, Application US/08556422A
 ; Patent No. 6576754
 ; GENERAL INFORMATION:
 ; APPLICANT: HALL, Kathryn T.
 ; APPLICANT: FREEMAN, Jordan J.
 ; APPLICANT: SCHULTZE, Joachim L.
 ; APPLICANT: BOUSSIORIS, Vassiliki
 ; APPLICANT: NADLER, Lee M.
 ; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES
 ; FILE REFERENCE: DFN-005CPA2
 ; CURRENT APPLICATION NUMBER: US/08/556,422A
 ; CURRENT FILING DATE: 1995-11-09
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 4
 ; LENGTH: 607
 ; TYPE: PRT
 ; ORGANISM: Mus musculus
 US-08-556-422A-4

Alignment Scores:

Pred. No.: 1,45E-74 Length: 607
 Score: 838.50 Matches: 210
 Percent Similarity: 49.84% Conservative: 106
 Best Local Similarity: 33.12% Mismatches: 249
 Query Match: 17.13% Indels: 69
 DB: 4 Gaps: 22

US-09-774-490-1 (1-2709) x US-08-556-422A-4 (1-607)

QY 356 AACAGCTCCAGTATCATACCTCTCTTTGGATGAGGACGAGTAGGCTGTATGTTGA 415
 Db 12 AsnIleSerAsnTyrThrAlaLeuLeuLeuSerGlnAspGlyLysThrLeuTyrValGly 31
 QY 416 GCAAGGATCACATATTTTCATTCGACCTGGTGTATATCAAG-----GAT 460
 Db 32 AlaArgGluAlaLeuPheAlaLeuAsn---SerAsnLeuSerPheLeuProGlyGlyGlu 50
 QY 461 TTTCAAGAGTTGTGTGGCCAGTATCTTACACGACGAGATGAATGCAAGTGGCTGGA 520
 Db 51 TyrGlnGluLeuLeuTrpSerAlaAspAlaAspArgLysGlnGlnCysSerPheLysGly 70
 QY 521 AAAGACATCCTGAAGAATGCTATTTTCATCAAGGTACTTAAAGGCATATAATCAGACT 580
 Db 71 LysAspProLysArgAspCysGlnAsnIleLysLeuLeuProLeuAsnSerSer 90
 QY 581 CACTGTGACGCTGTGGACGGGCTTTTCACCAATTTGCACATTCACATTCGAATGGA 640
 Db 91 HisLeuLeuThrCysGlyThrAlaAlaPheSerProLeuCysAlaTyrIleHisIleAla 110
 QY 641 CATCATCTCGAGACATATTTTAACTGGAG-----AACTCACATTTT 685
 Db 111 Ser-----PheThrLeuAlaGlnAspGluAlaGlyAsnValIleLeu 124
 QY 686 GAAACGGCGGTGGGAAGAGTCCATATGACCTAACCTGCTGACAGCATCCCTTTTAATA 745
 Db 125 GluAspGlyLysGlyHisCysProPheAspProAsnPheLysSerThrAlaLeuValVal 144
 QY 746 GATGAGAGATTATATCTGGAACGAGCTGATTTTATGGGCGAGACTTTGCTATCTTC 805
 Db 145 AspGlyGluLeuTyrThrGlyThrValSerSerPheGlnGlyAsnAspProAlaIleSer 164

QY 806 CGAACTCTTGGGACACACCCCAATCAGACAGACAGCATGATTCAGGTCGTCAT 865
 Db 165 ArgSerGlnSer---SerArgProThrLysThrGluSer---SerLeuAsnTrpLeuGln 182
 QY 866 GATCCAAAGTTCTATTAGTGCCACCTCATCTCAGAGAGT---GACATCTCT---GAA 916
 Db 183 AspProAlaPheValAlaSerAlaThrSerProGluSerLeuGlySerProIleGlyAsp 202
 QY 917 GATGACAAAGTATATCTTTTCTCCGTGAAAAATGCAATAGATGAGAGACACTCTGGA 976
 Db 203 AspAspLysIleTyrPhePheSerGluThrGlyGlnGluPheGluPheGluAsn 222
 QY 977 GCTACTCACCTAGATAGGTGAGATGATCAAGAAATGACTTTGGAGGGCACAGAGCTG 1036
 Db 223 ThrIleValSerArgValAlaArgValCysLysGlyAspGluGlyGluArgValLeu 242
 QY 1037 GTGAATAAATGACACATCTCTCAAGTCGTCTGATTTGCTCAGTCGACAGTCCAAAT 1096
 Db 243 GlnGlnArgTrpThrSerPheLeuLysAlaGlnLeuLeuCysSerArgPro---AspAsp 261
 QY 1097 GGCATTGACACTCATTTTGTATGAACTGCAGAGTATTCCTAATG-----AACTTTAA 1150
 Db 262 GlyPhePro-----PheAsnValLeuGlnAspValPheThrLeuAsnProAsnProGln 279
 QY 1151 GATCCTAAAAATCCAGTTGTATATGAGAGTGTTCACGACTTC-----AGTAAACATTTC 1204
 Db 280 AspTrpArgLysThrLeuSerIleGlyValPheThrSerGlnTrpHisArgGlyThrThr 299
 QY 1205 AAGGATCAGCCGTGTGTATGTATAGCATGAGTGTGAGAGGGTGTCTTCTGTGTTCA 1264
 Db 300 GluGlySerAlaIleCysValPheThrMetAsnAspValGlnLysAlaPheAspGlyLeu 319
 QY 1265 TATGCCACAGGATGAGCCAACTATCAATGGTGCCTTATCAAGGAAGATCCCTAT 1324
 Db 320 TyrLysLysValAsnArgGluThrGlnGlnTrpTyrThrGluThrHisGlnValProThr 339
 QY 1325 CCACGGCCAGAACTTGT-----CCACGCAAAACATTTGGTGGTTGACTCTCAAAAG 1378
 Db 340 ProArgProGlyAlaCysIleThrAsnSerAlaArgGluArgLysIleAsnSerSerLeu 359
 QY 1379 GACCTTCCTCATGATGTATACTTTTGCAGAAAGTCATCCAGCCATGTACATCCAGTG 1438
 Db 360 GlnLeuProAspArgValLeuAsnPheLeuLysAspHisPheLeuMetAspGlyGlnVal 379
 QY 1439 TTTCTATGAACATCGCCCAATAGTATGATCAAAACGGATGATAAATTATCAATTACACA 1498
 Db 380 -----ArgSerArgLeuLeuLeuGlnProArgAlaArgTyrGln-----Arg 394
 QY 1499 ATTGTCGTACACCGAGTGGATGCAGAGATGGACAGTATGATCTTATGTTTATCGGAACA 1558
 Db 395 ValAlaValHisArgValProGlyLeuHisSerThrTyrAspValLeuPheLeuGlyThr 414
 QY 1559 GATGTTGGGACCGTCTTAAAGTAGTTTCAATTCCTAAAGAGACTTGGTATGATTTAGAA 1618
 Db 415 GlyAspGlyArgLeuHisLysAlaValThrLeuSerSerArgValHis-----430
 QY 1619 GAGGTTCTGTGGAAGAAATGACAGTTTTTCGGGAACCGACTCTCTATTTTTCAGCAATGGAG 1678
 Db 431 -----IleIleGluGluLeuGlnIlePheProGlnGlyGlnProValGlnAsnLeuLeu 448
 QY 1679 CTTTCCACTAAGCAGCAACACTATATATTGGTTCAACGGCTGGGTTGCCAGCTCCCT 1738
 Db 449 LeuAspSerHisGlyGlyLeuLeuTyrAlaSerSerHisSerGlyValValGlnValPro 468
 QY 1739 TTACACCGGTGTATATTTACGGGAAAGCGTGTGCTGAGTGTTCCTCGCCCGAGACCTT 1798
 Db 469 ValAlaAsnCysSerLeuTyr---ProThrCysGlyAspCysLeuLeuAlaArgAspPro 487
 QY 1799 TACTGTCTTGGATGTTCTCTGCATGT-----TCTCGCTATTTCCTCATCTGCAAG 1849
 Db 488 TyrCysAlaTrpThrGlySerAlaCysArgLeuAlaSerLeuTyrGlnProAspLeuAla 507

QY 1850 AGAGCCACAGACAGACAGATATAGAAATGGAGACCCACTGACTCTCTTCCAGACTTA 1909
 Db 508 SerArgProTptThrGlnAspIleGluGlyAlaSerValLysGluLeuCysLysAsn-- 526
 QY 1910 CACCATGATATACCATGGCCACAGCCCTCAAGAGAGATCATCTATGCTGTAGAG-- 1966
 Db 527 -----SerSerTyrllysAlaArgPheLeuValProGlyLysPro 539
 QY 1967 -----AATAGTAGCACATTTTGGAAATCCAGTCCCAAGTGG 2002
 Db 540 CysLysGlnValGlnIleGlnProAsnThrValAsnThrLeuAlaCysProLeuLeuSer 559
 QY 2003 CAGAGAGCGCTGTCTATTGCGAATTCAGAGCGGAATGAGAGCGAAAGAGAGATC 2062
 Db 560 AsnLeuAlaThrArgLeuTrpValHisAsnGlyAlaProValAsnAlaSerAlaSerCys 579
 QY 2063 AGAGTGGGATGATCATATCATCAGGACAGATCAAGGCGCTTCTGCTACGTAGTCTACACAG 2122
 Db 580 ArgVal-----LeuProThrGlyAspLeuLeuValGlySer-----Gln 593
 QY 2123 AAGGATTCAGCAATTAATCTCTGCGATCGCGTGGAAATGGG 2164
 Db 594 GlnGlyLeuGlyValPheGlnCysTrpSerIleGluGly 607

RESULT 12

US-09-653-274-8
 ; Sequence 8, Application US/09653274
 ; Patent No. 6635742
 ; GENERAL INFORMATION:
 ; APPLICANT: Boyle, Bryan J
 ; APPLICANT: Yeung, George Y
 ; APPLICANT: Arterburn, Matthew C
 ; APPLICANT: Mize, Nancy K
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Drmanac, Radoje T
 ; TITLE OF INVENTION: Methods and Materials Relating to Semaphorin-Like
 ; TITLE OF INVENTION: Polypeptides and Polynucleotides
 ; FILE REFERENCE: HVS-23
 ; CURRENT APPLICATION NUMBER: US/09/653,274
 ; CURRENT FILING DATE: 2000-08-31
 ; PRIOR APPLICATION NUMBER: 09/491,404
 ; PRIOR FILING DATE: 2000-01-10
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 1070
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-653-274-8

Alignment Scores:
 Pred. No.: 2,73e-72 Length: 1070
 Score: 817.00 Matches: 206
 Percent Similarity: 47.54% Conservative: 113
 Best Local Similarity: 30.70% Mismatches: 233
 Query Match: 16.69% Indels: 119
 DB: 4 Gaps: 25

US-09-774-490-1 (1-2709) x US-09-653-274-8 (1-1070)

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 QY 404 CTGTATGTTGGACCAAGAGATCACATATTTTCATTGCGACCTCGTGTAAATATCAAGATTTT 463
 Db 53 LeuTyrlleAlaGlyArgAspGlnValTyThr-----ValAsnLeuAsnGluMet 69
 QY 464 -----CAAAAGATTGTGGCCAGTATCTTACACAGAGA 499
 Db 70 ProLysThrGluValIleProAsnLysLysLeuThrTrpArgSerArgGlnGlnAspArg 89

QY 500 GATGAATCGAGTGGCGTGGAAAGACATCTCTGAAAGATGTGCTAAATTTTCATCAAGGTA 559
 Db 90 GluAsnCysAlaMetLysGlyLysHis---LysAspGluCysHisAsnPheIleLysVal 108
 QY 560 CTTAAGGCATATAATACAGACTCAGCTGTACGCTGTGGAAACGGGGCTTTTCATCCAATT 619
 Db 109 PheValProArgAsnAspGluMetValPheValCysGlyThrAsnAlaPheAsnProMet 128
 QY 620 TGCACCTACATTTGAATTTGGACATCATCTCTGAGGACATATTTTAACTCGAGAACTCA 679
 Db 129 CysArgTy-----TyArgLeuSerThrLeu 137
 QY 680 CATTTTGA-----AACGGCGTGGAGAGCTCCATATGACCCCTAAGCTGCTG 727
 Db 138 GluTyArgGlyGluGluIleSerGlyLeuAlaArgCysProPheAspAlaArgGlnThr 157
 QY 728 ACAGCATCCCTTTTAAATAGAGAGAAATATATCTCTGGAAGCTGCAGCTGATTTATGGG 787
 Db 158 AsnValAlaLeuPheAlaAspGlyLysLeuTySerAlaThrValAlaAspPheLeuAla 177
 QY 788 CGAGACTTTTGTCTATCTCTCGAACTCTTGGGACCAACCAATCAGGACAGAGCAT 847
 Db 178 SerAspAlaValIleTyArgSerMetGlyAspGlySerAlaLeuArgThrIleLysTy 197
 QY 848 GATTCAGTGGCTCAATGATCCAAAGTTTCATTAGTGGCCACCTCATCTCAGAGAGTGC 907
 Db 198 AspSerLysTrpIleLysGluProHisPheLeu-----HisAlaIleGluTyGly--- 214
 QY 908 ATCTCTGAAGATGACAAAGTATCTTTTCTCTGGAATGCAATAGATGAGAGAACAC 967
 Db 215 -----AsnTyValTyPhePheArgGluIleAlaValGluHisAsnAsn 230
 QY 968 TCTGAAAAAGTACTACGCTAGATAGATAGATGCAAGATGCTTTGGAGGGAC 1027
 Db 231 LeuGlyLysAlaValTySerArgValAlaArgLysLysAsnAspMetGlyLys 250
 QY 1028 AGAGTCTCGTGAATAA---TGGACACATTCCTCAAGCTCGTCTGATTTGCTCAGTG 1084
 Db 251 GlnArgValLeuGluLysHisTrpThrSerPheLeuLysAlaArgLeuAsnCysSerVal 270
 QY 1085 CCAGGTCCAAATGGCATTCACACTCATTTTGTATGAATGTCAG-----GATCTATTC 1135
 Db 271 ProGlyAspProPhePhe-----TyPheAspValLeuGlnSerIleThrAspIle 288
 QY 1136 CTAATGAATTTAAGATCCTTAAATCCAGTGTATGATGGAGTCTTTACGACTTCCAGT 1195
 Db 289 GlnIleAsn-----GlyIleProThrValValGlyValPheThrThrGlnLeu 304
 QY 1196 AACATTTTCAAGGATCAGCGTGTATGTATGATGATGATGATGATGATGATGATGATGATG 1255
 Db 305 AsnSerIleProGlySerAlaValCysAlaPheSerMetAspAspIleGluLysValPhe 324
 QY 1256 CTTGTCATATATGCCACAGGATGAGCCCACTATCAATGG-----GTGCTTATCAA 1309
 Db 325 LysGlyArgPheLysGluGlnLysThrProAspSerValTrpThrAlaValPro---Glu 343
 QY 1310 GGAAGAGTCCCTTATCCAGCGCCAGAACTTGTGCCAGCAAAACATTTGGT---GGTTT 1366
 Db 344 AspLysValProLysProArgProGlyCysCysAlaLysHisGlyLeuAlaGluAlaTy 363
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 QY 1487 CAATTTACAAATTTGCTGTAGACCGAGTGGATGCAAGAGATGGACAGATGATGATGATG 1546
 Db 404 ArgLeuThrAlaIleSerValAspHisSerAlaGlyProTyGlnAsnTyThrValIle 423
 QY 1547 TTTATCGAAACAGATGTTGGACCGCTTCTTAAAGTAGTTTCAATTCCTTAAGGAGACTGG 1606

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QY 908 AATCCTCGAAGATGACAAAGATATATCTTTCTTCCGTGAAATGCAATAGATGAGAACAC 967
Db 215 -----AsnTyrValTyrPhePhePheArgGluIleAlaValGluHisAsnAsn 230
QY 968 TGTGAAAAGCTACTCACGCTAGATAGTGTGATGCAAGATGCAATGACCTTTGGAGGGCAC 1027
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Db 251 GlnArgValLeuGluLysHisTrpThrSerPheLeuLysAlaArgLeuAsnCysSerVal 270
QY 1085 CCAGGTCCAAATGGCATTGACACTCATTTTGTGATGACCTGAG-----CATGTATTC 1135
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QY 1196 AACATTTTCAAGGATCAGCGCTGTATGTATGATGATGATGATGATGATGATGATGATGATG 1255
Db 305 AsnSerIleProGlySerAlaValCysAlaPheSerMetAspAspIleGluLysValPhe 324
QY 1256 CTGTGTCCTATATGCCACAGGATGACCCCACTATCATG-----GTGCTTATCAA 1309
Db 325 LysGlyArgPheLysGluGlnLysThrProAspSerValTrpThrAlaValPro---Glu 343
QY 1310 GGAAGAGTCCCTATCCAGCGCAGGAACTTGTCCAGCAAAACATTTGCT---GGTTT 1366
Db 344 AspLysValProLysProArgProGlyCysAlaLysHisGlyLeuAlaGluAlaTyr 363
QY 1367 GACTCTACAAAGACCTCTCTGATGATGTTATACTTTGCAAGAGTCAATCCAGCCCATG 1426
Db 364 LysThrSerIleAspPheProaspGluThrLeuSerPheIleLysSerHisProLeuMet 383
QY 1427 TCAATCCAGTGTTCCTATGAAACAAATCCCAATAGTATGATCAAAACCGATGTAATAT 1486
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QY 1487 CAATTTACACAATTCGTAGACCCGAGTGGATGAGAGATGGACAGTATGATGATGATG 1546
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QY 1607 TATGATTTA---GAAGAGTTCCTGCTGGAGAAATGACAGTTT----- 1648
Db 442 PheSerLeuAsnAspSerValLeuLeuGluGluIleGluAlaTyrAsnHisAlaLysCys 461
QY 1649 -----CGGGAACCGACTGCTATTTCAGCAATGGAGCTTTCCTAAGCAGCA 1696
Db 462 SerAlaGluAsnGluAspLysLysValIleSerLeuGlnLeuAspLysAspHis 481
QY 1697 CAACTATATATGTTCAACGGCTGGGTGGTGGCCAGTCCCTTTACACCGTGTGATAT 1756
Db 482 AlaLeuTyrValAlaPheSerSerCysIleIleArgIleProLeuSerArgCysGluArg 501
QY 1757 TACGGGAAGCGTGTGCTGAGTGTGCTCGCCCGCAGACCTTACTGTGCTGG---CAT 1813
Db 502 TyrGlySerCysLysLysSerCysIleAlaSerArgAspProTyrCysGlyTrpLeuSer 521

QY 1814 GGTTCGATGTTCTCGCTATTTTCCACTGCAAGAGACGACCAAGA----- 1851
Db 522 GlnGlySerCysGlyArgValThrProGlyMetLeuLeuThrGluAspPhePheAla 541
QY 1862 -----CGACAAGATATAAGAAATGAGAGACCCACTGACT 1894
Db 542 PheHisAsnHisSerAlaGluGlyTyrGluGlnAspThrGluPheGlyAsn---ThrAla 560
QY 1895 CACTGTTTCAGACTTACACCATGATAATCACCATGGCCACAGCCCTGAGAGAGATCATC 1954
Db 561 HisLeuGlyAspCysHisGluIleLeuProThrSerThrProAspTyrLysIlePhe 580
QY 1955 TATGCT-----GTAGAGAATAGTACGACATTT 1981
Db 581 GlyGlyProThrSerAspMetGluValSerSerSerValThrThrMetAlaSerIle 600
QY 1982 TTGGAATGCGAGTCCGAAG 1999
Db 601 ProGluIleThrProLys 606
RESULT 15
US-08-121-713D-62
; Sequence 62, Application US/08121713D
; Patent No. 5639856
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713D
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 62:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 724 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-121-713D-62
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Pred. No.: 3,04e-69 Length: 724
Score: 785.50 Matches: 221
Percent Similarity: 47.48% Conservative: 118
Best Local Similarity: 30.95% Mismatches: 248
Query Match: 16.04% Indels: 127
DB: 1 Gaps: 30
US-09-774-490-1 (1-2709) x US-08-121-713D-62 (1-724)

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Job time : 116.5 secs

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GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 23, 2004, 01:19:05 ; Search time 1239 Seconds
(without alignments)
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Title: US-09-774-490-1

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Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3327077 seqs, 2523723180 residues

Total number of hits satisfying chosen parameters: 6654154

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:
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19: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
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2	2517	92.9	2848	15	US-10-247-671-83
3	2508.4	92.6	2530	15	US-10-097-340-283
4	2508.4	92.6	2530	15	US-10-262-538-9
5	2508.4	92.6	2601	15	US-10-067-632-53
6	718.6	26.5	2331	16	US-10-404-438-2
7	718.6	26.5	3871	10	US-09-946-374-309
8	718.6	26.5	3871	12	US-10-015-395A-309
9	718.6	26.5	3871	13	US-10-206-915-347
10	718.6	26.5	3871	13	US-10-199-670-347
11	718.6	26.5	3871	13	US-10-201-858-347
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13	718.6	26.5	3871	13	US-10-208-024-347
14	718.6	26.5	3871	13	US-10-201-853-347

15	718.6	26.5	3871	13	US-10-174-581-347	Sequence 347, App
16	718.6	26.5	3871	13	US-10-176-483-347	Sequence 347, App
17	718.6	26.5	3871	13	US-10-176-749-347	Sequence 347, App
18	718.6	26.5	3871	13	US-10-176-914-347	Sequence 347, App
19	718.6	26.5	3871	13	US-10-176-915-347	Sequence 347, App
20	718.6	26.5	3871	13	US-10-006-485A-309	Sequence 309, App
21	718.6	26.5	3871	13	US-10-013-907A-309	Sequence 309, App
22	718.6	26.5	3871	13	US-10-015-499A-309	Sequence 309, App
23	718.6	26.5	3871	13	US-10-176-484-347	Sequence 347, App
24	718.6	26.5	3871	13	US-10-180-550-347	Sequence 347, App
25	718.6	26.5	3871	13	US-10-183-014-347	Sequence 347, App
26	718.6	26.5	3871	13	US-10-187-738-347	Sequence 347, App
27	718.6	26.5	3871	13	US-10-187-740-347	Sequence 347, App
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33	718.6	26.5	3871	13	US-10-195-884-347	Sequence 347, App
34	718.6	26.5	3871	13	US-10-195-896-347	Sequence 347, App
35	718.6	26.5	3871	13	US-10-196-744-347	Sequence 347, App
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38	718.6	26.5	3871	13	US-10-197-704-347	Sequence 347, App
39	718.6	26.5	3871	13	US-10-197-710-347	Sequence 347, App
40	718.6	26.5	3871	13	US-10-198-758-347	Sequence 347, App
41	718.6	26.5	3871	13	US-10-198-766-347	Sequence 347, App
42	718.6	26.5	3871	13	US-10-199-304-347	Sequence 347, App
43	718.6	26.5	3871	13	US-10-199-309-347	Sequence 347, App
44	718.6	26.5	3871	13	US-10-199-313-347	Sequence 347, App
45	718.6	26.5	3871	13	US-10-199-456-347	Sequence 347, App

ALIGNMENTS

RESULT 1

US-09-774-490-1
; Sequence 1, Application US/09774490
; Patent No. US20010034332A1
; GENERAL INFORMATION:
; APPLICANT: Jin, Shengfang
; TITLE OF INVENTION: RESISTANCE SEQUENCES AND USES THEREOF
; FILE REFERENCE: 07334-138001
; CURRENT APPLICATION NUMBER: US/09/774,490
; PRIOR FILING DATE: 2001-01-31
; PRIOR APPLICATION NUMBER: US 60/179,191
; PRIOR FILING DATE: 2000-01-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 2709
; TYPE: DNA
; ORGANISM: Mus musculus
US-09-774-490-1

Query Match		100.0%	Score 2709;	DB 9;	Length 2709;
Best Local Similarity		100.0%	Pred. No. 0;		
Matches 2709;		Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
Qy	1	AATCTTTTATTTATCGATGTTAAACAGCTTAGTAATCGATGCCACGTCCAGGGGTGCG	60		
Db	1	AATCTTTTATTTATCGATGTTAAACAGCTTAGTAATCGATGCCACGTCCAGGGGTGCG	60		
Qy	61	ACCACGCGTCCGGGAGTAGTTGAGTTCCTCCATGTCACGAGTCTATTT	120		
Db	61	ACCACGCGTCCGGGAGTAGTTGAGTTCCTCCATGTCACGAGTCTATTT	120		
Qy	121	CCAGATGTTTGAACCTTCTTGCCGCCACAAATACAGAAAGAGACTAAAGCAGCAAGG	180		
Db	121	CCAGATGTTTGAACCTTCTTGCCGCCACAAATACAGAAAGAGACTAAAGCAGCAAGG	180		
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Q	y	361	 CTCCAGTTATCATACCTTCCCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTTGGAGCAAA	420
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Q	y	481	 AGTATCTTACACGAGAAGATGAATGCAAGTGGGCTGGAAAAAGACATCCTCGAAAGAATG	540
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Q	y	961	 AGAACACTCTCGAAAAGCTACTCAGCTAGAAATAGGTCAGATATGCAAGATGACTTTGG	1020
D	b	961	 AGAACACTCTCGAAAAGCTACTCAGCTAGAAATAGGTCAGATATGCAAGATGACTTTGG	1020
Q	y	1021	 AGGGCACAGAAAGTCTGGTGAATAATGGACAAATTCCTCAAAGCTCGTCTGATTGCTC	1080
D	b	1021	 AGGGCACAGAAAGTCTGGTGAATAATGGACAAATTCCTCAAAGCTCGTCTGATTGCTC	1080
Q	y	1081	 AGTGCCAGGTCCAAATGGCACTGACACTCATTTTGTATGAACTGCAAGATGATTTCTTAAT	1140
D	b	1081	 AGTGCCAGGTCCAAATGGCACTGACACTCATTTTGTATGAACTGCAAGATGATTTCTTAAT	1140
Q	y	1141	 GAACTTTTAAAGATCCTTAAATCCAGTTGTATATGGAGTGTTTACGACTCCAGTAAACAT	1200
D	b	1141	 GAACTTTTAAAGATCCTTAAATCCAGTTGTATATGGAGTGTTTACGACTCCAGTAAACAT	1200
Q	y	1201	 TTTCAAGGGATCAGCCGTGTGTATGTATAGCATGATGTGAGAAAGGTGTTCTCTGG	1260
D	b	1201	 TTTCAAGGGATCAGCCGTGTGTATGTATAGCATGATGTGAGAAAGGTGTTCTCTGG	1260
Q	y	1261	 TCCATATGCCACAGGGATGCAACCAACTATCAATGGGTGCCTTATCAAGGAAGAGTCCC	1320

Db	1261	TCATATGCCACACAGGATGGACCCAACTACTCAATGGGTGCCTTTATCAAGGAAGAGTGCC	1320
Qy	1321	CTATCCACGGCCAGGAACCTTGCCACAGCAAAACATTTGGTGGTTTTTGACTCTACAAAGGA	1380
Db	1321	CTATCCACGGCCAGGAACCTTGCCACAGCAAAACATTTGGTGGTTTTTGACTCTACAAAGGA	1380
Qy	1381	CGTTCTCGATGATGTATACCTTTCCAGAGAGTCATCCAGCCATGATCAATCCAGTGTT	1440
Db	1381	CGTTCTCGATGATGTATACCTTTCCAGAGAGTCATCCAGCCATGATCAATCCAGTGTT	1440
Qy	1441	TCCTATGAACAATCGCCCAATAGTGATCAAAACGGATGTAAATTTATCAATTTACACAAAT	1500
Db	1441	TCCTATGAACAATCGCCCAATAGTGATCAAAACGGATGTAAATTTATCAATTTACACAAAT	1500
Qy	1501	TGTCGTAGACGAGTGGATCGAGAAGATCGACAGTATGATGTATGTTTATTCGGAACAGA	1560
Db	1501	TGTCGTAGACGAGTGGATCGAGAAGATCGACAGTATGATGTATGTTTATTCGGAACAGA	1560
Qy	1561	TGTTGGGACCGTCTTTAAAGTAGTTCATTCCTAAGGAGACTTGGTATGATTTAGAAGA	1620
Db	1561	TGTTGGGACCGTCTTTAAAGTAGTTCATTCCTAAGGAGACTTGGTATGATTTAGAAGA	1620
Qy	1621	GGTTCGTGCGAAGAAATGACAGTTTTTCGGGAACCGACTGCTATTTTCAGCAATGAGACT	1680
Db	1621	GGTTCGTGCGAAGAAATGACAGTTTTTCGGGAACCGACTGCTATTTTCAGCAATGAGACT	1680
Qy	1681	TTCCAATAAGCAGCAACAACCTATATATGTGTTCAACGGCTGGGTTGCCAGCTCCCTTT	1740
Db	1681	TTCCAATAAGCAGCAACAACCTATATATGTGTTCAACGGCTGGGTTGCCAGCTCCCTTT	1740
Qy	1741	ACACCGGTGTCATATTTACCGGAACCGGTGCTGAGTGTTCCTCGCCCGGAGACCCCTTA	1800
Db	1741	ACACCGGTGTCATATTTACCGGAACCGGTGCTGAGTGTTCCTCGCCCGGAGACCCCTTA	1800
Qy	1801	CTGTGCTTGGGATGGTTCTGCATGTTCTCGCTATTTTCCACTGCAAGAGACGCAACAG	1860
Db	1801	CTGTGCTTGGGATGGTTCTGCATGTTCTCGCTATTTTCCACTGCAAGAGACGCAACAG	1860
Qy	1861	ACGCAAGATATAGAANAATGGAGACCCACTGACTCTGTTCAGACTTTACACCATGATAA	1920
Db	1861	ACGCAAGATATAGAANAATGGAGACCCACTGACTCTGTTCAGACTTTACACCATGATAA	1920
Qy	1921	TCACCATGGCCACAGCCCTGAAAGAGAAATCATCTATATGTTGATAGAAATAGTAGCAATT	1980
Db	1921	TCACCATGGCCACAGCCCTGAAAGAGAAATCATCTATGTTGATAGAAATAGTAGCAATT	1980
Qy	1981	TTTGGAAATGCAGTCCGAAGTCGCAGAGAGCGGTGCTTATTGGCAATTCAGAGCGCAAA	2040
Db	1981	TTTGGAAATGCAGTCCGAAGTCGCAGAGAGCGGTGCTTATTGGCAATTCAGAGCGCAAA	2040
Qy	2041	TGAAGCGGAAAAGAGAGATCAGAGTGATGATCATATCATCAGACAGATCAAGGCT	2100
Db	2041	TGAAGCGGAAAAGAGAGATCAGAGTGATGATCATATCATCAGACAGATCAAGGCT	2100
Qy	2101	TCGTGACTGCTAGTCTCAACAGAAAGATTACAGCAATTTACCTTCGCATGCGGTGGAACA	2160
Db	2101	TCGTGACTGCTAGTCTCAACAGAAAGATTACAGCAATTTACCTTCGCATGCGGTGGAACA	2160
Qy	2161	TGGGTTCATCAAACTCTTCTTAAGGTATACCTTGAAGTCAATTGACACAGAGCATTTGGA	2220
Db	2161	TGGGTTCATCAAACTCTTCTTAAGGTATACCTTGAAGTCAATTGACACAGAGCATTTGGA	2220
Qy	2221	AGAACTTCTTCATAAAGATGATGATGGAGATGGCTCTTAAGACCAAGAAATGTCCCAATAG	2280
Db	2221	AGAACTTCTTCATAAAGATGATGATGGAGATGGCTCTTAAGACCAAGAAATGTCCCAATAG	2280
Qy	2281	CATGACCTTAGCCAGAGGCTTGTTGACAGAGACTTCTATGAGCTCATCAACCAACCCCA	2340
Db	2281	CATGACCTTAGCCAGAGGCTTGTTGACAGAGACTTCTATGAGCTCATCAACCAACCCCA	2340
Qy	2341	TCTCAACAAGATGGATGAGTTCGTGAAACAAGTTTGGHAAAAGGACCCGAAAAACAAGTCG	2400
Db	2341	TCTCAACAAGATGGATGAGTTCGTGAAACAAGTTTGGHAAAAGGACCCGAAAAACAAGTCG	2400

QY 2401 GCAAGGCCAGACATACCCAGGGAACAGTAAACAAATGGAGACATTTACAGAAATAA 2460
Db 2401 GCAAGGCCAGACATACCCAGGGAACAGTAAACAAATGGAGACATTTACAGAAATAA 2460
QY 2461 GAAAGGTAGAAACAGGAGGACCCAGCAATTTGAGAGGACACCCAGGAGTGTCTGAGCTGC 2520
Db 2461 GAAAGGTAGAAACAGGAGGACCCAGCAATTTGAGAGGACACCCAGGAGTGTCTGAGCTGC 2520
QY 2521 ATTACTCTAGAAACCTCAACAGTAGAATACTTGCCTAGACATATACTGGAACAAACAA 2580
Db 2521 ATTACTCTAGAAACCTCAACAGTAGAATACTTGCCTAGACATATACTGGAACAAACAA 2580
QY 2581 TGCAATATACATGAACATTTTTCATGCGATTATGCGATGTTTACAATGCGGGAATTC 2640
Db 2581 TGCAATATACATGAACATTTTTCATGCGATTATGCGATGTTTACAATGCGGGAATTC 2640
QY 2641 AGCTGAGTTCACCAATATATAATTAATCCATGAGTAACTTCTTAATAGGCTTTTTT 2700
Db 2641 AGCTGAGTTCACCAATATATAATTAATCCATGAGTAACTTCTTAATAGGCTTTTTT 2700
QY 2701 CCTAATACC 2709
Db 2701 CCTAATACC 2709

RESULT 2
US-10-247-671-83
; Sequence 83, Application US/10247671
; Publication No. US20030194721A1
; GENERAL INFORMATION:
; APPLICANT: Mikita, Thomas
; APPLICANT: Shiffman, Dov
; APPLICANT: Porter, Gordon, J.
; APPLICANT: Kaser, Matthew R.
; TITLE OF INVENTION: GENES EXPRESSED IN TREATED FOAM CELLS
; FILE REFERENCE: PA-0050 US
; CURRENT APPLICATION NUMBER: US/10/247,671
; CURRENT FILING DATE: 2002-09-18
; PRIOR APPLICATION NUMBER: 60/323,784
; PRIOR FILING DATE: 2001-09-19
; NUMBER OF SEQ ID NOS: 186
; SOFTWARE: PERL Program
; SEQ ID NO 83
; LENGTH: 2848
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20030194721A1 1930967CB1
US-10-247-671-83

Query Match 92.9%; Score 2517; DB 15; Length 2848;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 193 CTGAGCATGGCTGGTTAACTAGGATGCTGCTCTTTCTGGGGAGTATTACTTACAGC 252
Db 9 CTGAGCATGGCTGGTTAACTAGGATGCTGCTCTTTCTGGGGAGTATTACTTACAGC 68
QY 253 AAGAGCAAACTATCAGAAATGGAGAAACAAATGCGCAGGCTGAAATTTCTCTACAAAGA 312
Db 69 AAGAGCAAACTATCAGAAATGGAGAAACAAATGCGCAGGCTGAAATTTCTCTACAAAGA 128
QY 313 AATGTTGGAATCCAAACAAATGATGATCACTTCAATGGCTTGGCCCAACAGCTCCAGTTATCA 372
Db 129 AATGTTGGAATCCAAACAAATGATGATCACTTCAATGGCTTGGCCCAACAGCTCCAGTTATCA 188
QY 373 TACCTTCCTTTGGATGAGGAACGAGTAGGCTGTATGTTGGAGCAAGGATCACATATT 432
Db 189 TACCTTCCTTTGGATGAGGAACGAGTAGGCTGTATGTTGGAGCAAGGATCACATATT 248
QY 433 TTCATTGCACTGGTGTAAATCAAGGATTTTCAAAAGANTTTGTGTGCCAGTATCTTACAC 492

Db 249 TTCAATTCGACCTGGTTAAATATCAAGGATTTTCAAAAGATTTGTGTGCCAGTATCTTACAC 308
QY 493 CAGAAGAGATGAATCAAGTGGCTCGAAAAGACATCTCTGAAAAGATGTCTAAATTCAT 552
Db 309 CAGAAGAGATGAATCAAGTGGCTCGAAAAGACATCTCTGAAAAGATGTCTAAATTCAT 368
QY 553 CAAGGTACTTAAAGCATATAATCAGACTCACTTGTACGCTGTGGAAACGGGGCTTTTCA 612
Db 369 CAAGGTACTTAAAGCATATAATCAGACTCACTTGTACGCTGTGGAAACGGGGCTTTTCA 428
QY 613 TCCAAATTTGACCTCACTTGAATTTGACATCATCTGAGGACAAATATTTTAAAGCTGGA 672
Db 429 TCCAAATTTGACCTCACTTGAATTTGACATCATCTGAGGACAAATATTTTAAAGCTGGA 488
QY 673 GAATCACTATTTGAAAAACGGCGTGGGAAGAGTCCATATGACCTTAAGCTGTGACAGC 732
Db 489 GAATCACTATTTGAAAAACGGCGTGGGAAGAGTCCATATGACCTTAAGCTGTGACAGC 548
QY 733 ATCCCTTTTAAATAGATGGAGAAATTAATCTGGAACCTGAGCTGATTTTATGGGGGAGA 792
Db 549 ATCCCTTTTAAATAGATGGAGAAATTAATCTGGAACCTGAGCTGATTTTATGGGGGAGA 608
QY 793 CTTTGTCTATCTCCGAACTCTTGGGCAACCAACCAATCAGGACAGACAGCATGATTC 852
Db 609 CTTTGTCTATCTCCGAACTCTTGGGCAACCAACCAATCAGGACAGACAGCATGATTC 668
QY 853 CAGGTGCTCAATGATCCAAAGTTCATTTAGTCCCACTCTCTCAGAGAGTGACATCC 912
Db 669 CAGGTGCTCAATGATCCAAAGTTCATTTAGTCCCACTCTCTCAGAGAGTGACATCC 728
QY 913 TGAAGATGACAAAGTATACCTTTTCTCGTGAAAATGCAATAGATGGAGAACATCTCTGG 972
Db 729 TGAAGATGACAAAGTATACCTTTTCTCGTGAAAATGCAATAGATGGAGAACATCTCTGG 788
QY 973 AAAAGCTACTCAGCTAGAAATAGTGCAGATATGCAAGAAATGATTTGGAGGGCACAGAAG 1032
Db 789 AAAAGCTACTCAGCTAGAAATAGTGCAGATATGCAAGAAATGATTTGGAGGGCACAGAAG 848
QY 1033 TCTGTTGAATTAATGACAAACATTTCTCAAAGCTGCTGATTTGCTCAGTGCAGGCTCC 1092
Db 849 TCTGTTGAATTAATGACAAACATTTCTCAAAGCTGCTGATTTGCTCAGTGCAGGCTCC 908
QY 1093 AAATGGCATGACATCACTTTTGTGAACTGAGATGATTTCTTAATGAACTTTAAAGA 1152
Db 909 AAATGGCATGACATCACTTTTGTGAACTGAGATGATTTCTTAATGAACTTTAAAGA 968
QY 1153 TCCTTAAATCCAGTTGTATATGGAGTGTTCAGCTTCCAGTAAACATTTTCAAGGATC 1212
Db 969 TCCTTAAATCCAGTTGTATATGGAGTGTTCAGCTTCCAGTAAACATTTTCAAGGATC 1028
QY 1213 AGCGTGTGTATGTATAGCATGATGTGAGAGGGTGTTCCTTGTCTCATATGCCCA 1272
Db 1029 AGCGTGTGTATGTATAGCATGATGTGAGAGGGTGTTCCTTGTCTCATATGCCCA 1088
QY 1273 CAGGAGTGAACCAACTATCAATGGTGCCTTATCAAGGAAGTCCCTATCCAGGCTC 1332
Db 1089 CAGGAGTGAACCAACTATCAATGGTGCCTTATCAAGGAAGTCCCTATCCAGGCTC 1148
QY 1333 AGGAATCTTCCAGCAAAACATTTTGTGTTTCACTCTACAAAGGACCTTCTCTGATCA 1392
Db 1149 AGGAATCTTCCAGCAAAACATTTTGTGTTTCACTCTACAAAGGACCTTCTCTGATCA 1208
QY 1393 TGTATAACCTTTGGAAGAGTCACTCCAGCCCATGTAATCAATCAAGTGTTCCTATGAACAA 1452
Db 1209 TGTATAACCTTTGGAAGAGTCACTCCAGCCCATGTAATCAATCAAGTGTTCCTATGAACAA 1268
QY 1453 TCGCCCAATAGTATCAAAACGGATGTAATTTATCAATTTACAAATTTGCTAGACCG 1512
Db 1269 TCGCCCAATAGTATCAAAACGGATGTAATTTATCAATTTACAAATTTGCTAGACCG 1328
QY 1513 AGTGAATGCAAGATGGACAGTATGTTTATGTTTATCGGAACAGATGTTGGGACCGT 1572

QY	433	TTCAATTCGACCTGGTTAAATATCAAGGATTTTCAAGAATTTGTGCGCCAGTATCTTACAC	492	1513	AGTGGATGCGAAGATGCGACGATGATGATGTTTATCGGAACAGATGTTGGGACCGT	1572
Db	249	TTTTTCGACCTGGTTTAAATATCAAGGATTTTCAAGAATTTGTGCGCCAGTATCTTACAC	308	1329	AGTCGATGCGAAGATGCGACGATGATGATGTTTATCGGAACAGATGTTGGGACCGT	1388
QY	493	CAGAAGAGATGAATGCAAGTGGCTGGAAAGACACATCTCTGAAAGAAATGTGCTAAATTCAT	552	1573	TCCTTAAAGTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAAAGAGTTCTGCTGGA	1632
Db	309	CAGAAGAGATGAATGCAAGTGGCTGGAAAGACACATCTCTGAAAGAAATGTGCTAAATTCAT	368	1389	TCCTTAAAGTAGTTTCAATTCCTAAGGAGACTTGGTATGATTTAGAAAGAGTTCTGCTGGA	1448
QY	553	CAAGGTACTTAAGGCATATAAATCAGACTCAGTTGTACGCTGTGAAAGGGGGCTTTTCA	612	1633	AGAAATGACAGTATTTTTCGGGAACCGACTGCTATTTTCAGCAATGAGCTTTCCACTAAGCA	1692
Db	369	CAAGGTACTTAAGGCATATAAATCAGACTCAGTTGTACGCTGTGAAAGGGGGCTTTTCA	428	1449	AGAAATGACAGTATTTTTCGGGAACCGACTGCTATTTTCAGCAATGAGCTTTCCACTAAGCA	1508
QY	613	TCCAAATTTGCACCTACATTTGGAATTTGGACATCATCTGAGGACAAATATTTTAAAGCTGGA	672	1693	GCAACAACTATATATGTTTCAAGCGCTGGGTGGCTGCTGCTCGGCCGAGAGCCCTTACTGTCTGGGA	1752
Db	429	TCCAAATTTGCACCTACATTTGGAATTTGGACATCATCTGAGGACAAATATTTTAAAGCTGGA	488	1509	GCAACAACTATATATGTTTCAAGCGCTGGGTGGCTGCTGCTCGGCCGAGAGCCCTTACTGTCTGGGA	1568
QY	673	GAACTCAGATTTTGAAGCGCGGTGGGAAGTCCATATGACCTTAAGCTGTGACAGC	732	1753	TATTTACGGGAAAGCGTGTGCTGAGTGTGCTCTCGCCGAGACCCCTTACTGTCTGGGA	1812
Db	489	GAACTCAGATTTTGAAGCGCGGTGGGAAGTCCATATGACCTTAAGCTGTGACAGC	548	1569	TATTTACGGGAAAGCGTGTGCTGAGTGTGCTCTCGCCGAGAGCCCTTACTGTCTGGGA	1628
QY	733	ATCCCTTTTAAATAGATGAGAAATATATCTCTGGAATCTGAGTGAATTTTATGGGCGGAGA	792	1813	TGGTTCGTCATGTTCTCGCTATTTTCCACTGCAAGAGACGACACAGAGCAAGATAT	1872
Db	549	ATCCCTTTTAAATAGATGAGAAATATATCTCTGGAATCTGAGTGAATTTTATGGGCGGAGA	608	1629	TGGTTCGTCATGTTCTCGCTATTTTCCACTGCAAGAGACGACACAGAGCAAGATAT	1688
QY	793	CTTTGCTATCTTCCGAATCTTTGGGACACACACCAATCAGGACAGAGCAGCATGATTC	852	1873	AAGAAATGAGAGACCCACTGACTCACTGTTTACAGACTTTACACCATGATAATCACCATGGCCA	1932
Db	609	CTTTGCTATCTTCCGAATCTTTGGGACACACACCAATCAGGACAGAGCAGCATGATTC	668	1689	AAGAAATGAGAGACCCACTGACTCACTGTTTACAGACTTTACACCATGATAATCACCATGGCCA	1748
QY	853	CAGGTGGCTCAATGATCCAAAGTTCATTAGTGGCCACCTCATCTCAGAGAGTGCAATCC	912	1933	CAGCCCTGAAGAGAGATCATCTATGGTGTAGAGATAGTAGACATTTTGGAAATGCGAG	1992
Db	669	CAGGTGGCTCAATGATCCAAAGTTCATTAGTGGCCACCTCATCTCAGAGAGTGCAATCC	728	1749	CAGCCCTGAAGAGAGATCATCTATGGTGTAGAGATAGTAGACATTTTGGAAATGCGAG	1808
QY	913	TGAAGATGACAAAGTATATCTTTTCTCCGTGAAATGCAATAGATGAGAGACACTCTGG	972	1993	TCCGAAGTCCGACAGAGCGCTGGTCTTATTTGGCAATTTCCAGAGCGGAAATGAAGAGCGAAA	2052
Db	729	TGAAGATGACAAAGTATATCTTTTCTCCGTGAAATGCAATAGATGAGAGACACTCTGG	788	1809	TCCGAAGTCCGACAGAGCGCTGGTCTTATTTGGCAATTTCCAGAGCGGAAATGAAGAGCGAAA	1868
QY	973	AAAAGCTACTCAGCTAGATAGTGCAGATATGCAAGATAGACTTTGGAGGGGACAGAG	1032	2053	AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTACGTAG	2112
Db	789	AAAAGCTACTCAGCTAGATAGTGCAGATATGCAAGATAGACTTTGGAGGGGACAGAG	848	1869	AGAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTACGTAG	1928
QY	1033	TCTGTGTAATTAATGGACAAATCTCTCAAGCTCGTCTGATTTGCTCAGTGCCAGGTCC	1092	2113	TCTTACAAAGAGAGATTCAGGCAATTCCTCTGCCATGCGGTGGAGACATGGTTCATACA	2172
Db	849	TCTGTGTAATTAATGGACAAATCTCTCAAGCTCGTCTGATTTGCTCAGTGCCAGGTCC	908	1929	TCTTACAAAGAGAGATTCAGGCAATTCCTCTGCCATGCGGTGGAGACATGGTTCATACA	1988
QY	1093	AAATGGCATGACATCTATTTGATGAATCAGGATGATTTCCCTAATGAATCTTTAAAGA	1152	2173	AACTCTTCTTTAAGTTAACTTGAAGTCAATGACACAGAGCATTTTGGAAAGAACTTTCTTCA	2232
Db	909	AAATGGCATGACATCTATTTGATGAATCAGGATGATTTCCCTAATGAATCTTTAAAGA	968	1989	AACTCTTCTTTAAGTTAACTTGAAGTCAATGACACAGAGCATTTTGGAAAGAACTTTCTTCA	2048
QY	1153	TCCTAAATCCAGTTGATATGAGTGTGTTTACGACTTCCAGTAAACATTTTCAAGGATC	1212	2233	TAAAGATGATGATGGAGATGGCTCTTAAGACCAAGAAATGTCCAATAGCATGACACCTAG	2292
Db	969	TCCTAAATCCAGTTGATATGAGTGTGTTTACGACTTCCAGTAAACATTTTCAAGGATC	1028	2049	TAAAGATGATGATGGAGATGGCTCTTAAGACCAAGAAATGTCCAATAGCATGACACCTAG	2108
QY	1213	AGCCGTGTATGTATAGCATGAGTGTGAGAGGGGTGTTTCTTGTCCATATGCCCA	1272	2293	CCAGAAGGTCCTGGTACAGAGACTTTCATGAGCTTCATCAACACCCCAATCTCAACACGAT	2352
Db	1029	AGCCGTGTATGTATAGCATGAGTGTGAGAGGGGTGTTTCTTGTCCATATGCCCA	1088	2109	CCAGAAGGTCCTGGTACAGAGACTTTCATGAGCTTCATCAACACCCCAATCTCAACACGAT	2168
QY	1273	CAGGATGACCCCACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTTATCCACGGCC	1332	2353	GGATGATGTTCTGTGAACAAGTTTGGAAAGGGGACCGGAAACAAAGCTGCGCAAGGCCAGG	2412
Db	1089	CAGGATGACCCCACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTTATCCACGGCC	1148	2169	GGATGATGTTCTGTGAACAAGTTTGGAAAGGGGACCGGAAACAAAGCTGCGCAAGGCCAGG	2228
QY	1333	AGGAATCTGTCCAGCAAAAATTTGGTGGTTTGTGACTCTCAAGAGGACCTTCTCTGATGA	1392	2413	ACATACCCCAAGGAAACAGTAAACAAATGGAAGCACTTACAAAGAAATTAAGAAAGGTAGAAA	2472
Db	1149	AGGAATCTGTCCAGCAAAAATTTGGTGGTTTGTGACTCTCAAGAGGACCTTCTCTGATGA	1208	2229	ACATACCCCAAGGAAACAGTAAACAAATGGAAGCACTTACAAAGAAATTAAGAAAGGTAGAAA	2288
QY	1393	TGTTATAACCTTTGCAAGAGTCAATCCAGCATGTACAAATCCAGTGTTCCTATGAACAA	1452	2473	CAGGAGGACCCAGAAATTTGAGAGGGACCCAGGAGTGTCTGAGCTGCAATACCTCTAGA	2532
Db	1209	TGTTATAACCTTTGCAAGAGTCAATCCAGCATGTACAAATCCAGTGTTCCTATGAACAA	1268	2289	CAGGAGGACCCAGAAATTTGAGAGGGACCCAGGAGTGTCTGAGCTGCAATACCTCTAGA	2348
QY	1453	TCGCCAATAGTATCAAAAAGGATGAAATTTATCAATTTTACAAAATTCGCTGAGACCG	1512	2533	AACTCAAAACAGTAGAAACTTGGCTTAGACAATACTGGAAACAAATTCGAATATACAT	2592
Db	1269	TCGCCAATAGTATCAAAAAGGATGAAATTTATCAATTTTACAAAATTCGCTGAGACCG	1328	2349	AACTCAAAACAGTAGAAACTTGGCTTAGACAATACTGGAAACAAATTCGAATATACAT	2408
				2593	GAACTTTTTCATGGCAATATGTTGATGTTTCAATGTTGGGAAATTCAGCTGAGTTCCA	2652

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Db 2409 GAACTTTTTCATGGCAATATGATGATGTTTCAATAGTGGGAAATTCAGCTGATTC 2468
Qy 2653 CCAATTATAAATTAATCCATGAGTAACCTTCTCTAATAGGCTTTTTC 2702
Db 2469 CCAATTATAAATTAATCCATGAGTAACCTTCTCTAATAGGCTTTTTC 2518

RESULT 4
US-10-262-538-9
; Sequence 9, Application US/10262538
; Publication No. US200301133241
; GENERAL INFORMATION:
; APPLICANT: Alitalo et al
; TITLE OF INVENTION: NEUROPILIN/VEGF-C/VEGFR-3 MATERIALS AND METHODS
; FILE REFERENCES: 28967/37564
; CURRENT APPLICATION NUMBER: US/10/262,538
; CURRENT FILING DATE: 2002-09-30
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 9
; LENGTH: 2530
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (16)..(2331)
US-10-262-538-9

Query Match 92.6%; Score 2508.4; DB 15; Length 2530;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 193 CTCGACATGGGCTGGTAACTAGGATGTCGTCTTTCTGGGAGTATTACTTACAGC 252
Db 9 CTCGACATGGGCTGGTAACTAGGATGTCGTCTTTCTGGGAGTATTACTTACAGC 68

Qy 253 AGAGCAAACTATCGAATGGGAAGCAAAATGTCGACGCTGAAATTCCTACAGA 312
Db 69 AGAGCAAACTATCGAATGGGAAGCAAAATGTCGACGCTGAAATTCCTACAGA 128

Qy 313 AATGTTGGAATCAACAATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCA 372
Db 129 AATGTTGGAATCAACAATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCA 188

Qy 373 TACCTCTCTTTGGATGAGGAACGAGTAGGCTGTATGTTGGACAAAGATCACATTT 432
Db 189 TACCTCTCTTTGGATGAGGAACGAGTAGGCTGTATGTTGGACAAAGATCACATTT 248

Qy 433 TTCATTTCGACCTGGTTAATATATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACAC 492
Db 249 TTCATTTCGACCTGGTTAATATATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACAC 308

Qy 493 CAGAAGAGATGAATCGAAGTGGCTGGAAAGACATCTCTGAAAGATGTGCTAATTTTCAT 552
Db 309 CAGAAGAGATGAATCGAAGTGGCTGGAAAGACATCTCTGAAAGATGTGCTAATTTTCAT 368

Qy 553 CAAGGTACTTAAGGCATATAATCAGACTCACTTGTACGCTTGTGGAAACGGGGCTTTTCA 612
Db 369 CAAGGTACTTAAGGCATATAATCAGACTCACTTGTACGCTTGTGGAAACGGGGCTTTTCA 428

Qy 613 TCCAAATTCGACCTACATGAATTTGACATCATCTTGGACAAATTTTAAAGCTGGA 672
Db 429 TCCAAATTCGACCTACATGAATTTGACATCATCTTGGACAAATTTTAAAGCTGGA 488

Qy 673 GAACCTCACAATTTGAAACGGCGGTGGGAAGAGTCCATATCACCTTAAGCTGTGACAGC 732
Db 489 GAACCTCACAATTTGAAACGGCGGTGGGAAGAGTCCATATCACCTTAAGCTGTGACAGC 548

Qy 733 ATCCCTTTTAAATAGATGGGAATTTACTCTGGAACTGCACTGATTTTATGGGGGAGA 792
Db 549 ATCCCTTTTAAATAGATGGGAATTTACTCTGGAACTGCACTGATTTTATGGGGGAGA 608

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Qy 793 CTTTCTATCTTCCGAACCTCTTGGGACCAACCCCAATCAGGACAGAGCAGCATGATTC 852
Db 609 CTTTCTATCTTCCGAACCTCTTGGGACCAACCCCAATCAGGACAGAGCAGCATGATTC 668
Qy 853 CAGGTGGCTCAATGATCCAAAGTTTCAATAGTCCCACTCATCTCAGAGAGTGCACAAATCC 912
Db 669 CAGGTGGCTCAATGATCCAAAGTTTCAATAGTCCCACTCATCTCAGAGAGTGCACAAATCC 728
Qy 913 TGAAGATGACAAAGATATATCTTTTCTTCCGTAATAATGCAATAGATGGAGAACATCTCTGG 972
Db 729 TGAAGATGACAAAGATATATCTTTTCTTCCGTAATAATGCAATAGATGGAGAACATCTCTGG 788
Qy 973 AAAAGCTACTCAGCTAGATAGGTGAGATATGCAAGAAATGACTTTTGGAGGGCACAGAAG 1032
Db 789 AAAAGCTACTCAGCTAGATAGGTGAGATATGCAAGAAATGACTTTTGGAGGGCACAGAAG 848
Qy 1033 TCTGTGTAATAATGAGCAACATTTCTCAAAGCTGCTGATTTGCTGCTCAGTCCAGGTCC 1092
Db 849 TCTGTGTAATAATGAGCAACATTTCTCAAAGCTGCTGATTTGCTGCTCAGTCCAGGTCC 908
Qy 1093 AAATGCGCATTCGACACTCATTTTGTATGAATGCAAGATGATTTCTAATGAATTTTAAAGA 1152
Db 909 AAATGCGCATTCGACACTCATTTTGTATGAATGCAAGATGATTTCTAATGAATTTTAAAGA 968
Qy 1153 TCCTAAAAATCCAGTTGTATATGAGTGTTTTACGACTTCCAGTAACATTTTCAAGGATC 1212
Db 969 TCCTAAAAATCCAGTTGTATATGAGTGTTTTACGACTTCCAGTAACATTTTCAAGGATC 1028
Qy 1213 AGCCGTGTATGATATAGCATGAGTGTGAGAGAGGTGTTCTCTGGTCCATATGCCCA 1272
Db 1029 AGCCGTGTATGATATAGCATGAGTGTGAGAGAGGTGTTCTCTGGTCCATATGCCCA 1088
Qy 1273 CAGGATGGAACCAACTATCAATGGTGCCTTATCAAGGAAGAGTCCCTTATCCAGGGCC 1332
Db 1089 CAGGATGGAACCAACTATCAATGGTGCCTTATCAAGGAAGAGTCCCTTATCCAGGGCC 1148
Qy 1333 AGGAACCTTGTCCAGCAAAACATTTGGTGGTGTGACTCTACAAAGAGCTTCTCTATGA 1392
Db 1149 AGGAACCTTGTCCAGCAAAACATTTGGTGGTGTGACTCTACAAAGAGCTTCTCTATGA 1208
Qy 1393 TGTATTAACCTTGTCCAGCAAAACATTTGGTGGTGTGACTCTACAAAGAGCTTCTCTATGA 1452
Db 1209 TGTATTAACCTTGTCCAGCAAAACATTTGGTGGTGTGACTCTACAAAGAGCTTCTCTATGA 1268
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Qy 1513 AGTGGATGCAAGAGATGGAAGTATGATGTTTATCGGAACAGATGTTGGGACCGT 1572
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Db 1389 TCTTAAAGTATGTTCAATTTCTAAGGAGACTTGTATGATTTAGAGAGAGTCTGCTGGA 1448
Qy 1633 AGAAATGACAGTCTTTCGGGAAACCGACTGCTATTTTTCAGCAATGAGCTTTCACATGA 1692
Db 1449 AGAAATGACAGTCTTTCGGGAAACCGACTGCTATTTTTCAGCAATGAGCTTTCACATGA 1508
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Db 1509 GCAACACTATATATGTTTCAAGGCTGGGTTTGGCCAGCTCCCTTTACACGGGTGCA 1568
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Db 1569 TATTTACGGGAAACCGTGTGCTGAGTGTGCTTCCCTGCGCCGAGACCTTACTGTCTTGGGA 1628
Qy 1813 TGGTTCGCAATGTTCTGCTATTTTCCACTGCAAAAGAGAGCGCACAAAGAGCAAGATAT 1872
Db 1629 TGGTTCGCAATGTTCTGCTATTTTCCACTGCAAAAGAGAGCGCACAAAGAGCAAGATAT 1688
Qy 1873 AAGAAATGGAGACCACTGACTCACTGCTTCACTTACACATGATAATCACCATGGGCA 1932

```

DB	1589	AAGAAATGGAGACCCACTGATCTACTGTTCAGACTTACCATGATAATCACCATGGCCA	1748
QY	1933	CAGCCCTGAAGAGAGAATCATCTATGTGTGAGAAATAGTAGACATTTTGGAAATCGAG	1992
DB	1749	CAGCCCTGAAGAGAGAATCATCTATGTGTGAGAAATAGTAGACATTTTGGAAATCGAG	1808
QY	1993	TCCGAAGTCGAGAGAGCGGTGGTCTATTGGCAATCCAGAGGCGAAATGAAGAGCGAAA	2052
DB	1809	TCCGAAGTCGAGAGAGCGGTGGTCTATTGGCAATCCAGAGGCGAAATGAAGAGCGAAA	1868
QY	2053	AGAAAGATCAGAGCTGGATGATCATATCATCAGGACAGATCAAGGCCCTTCGTCTAGTAG	2112
DB	1869	AGAAAGATCAGAGCTGGATGATCATATCATCAGGACAGATCAAGGCCCTTCGTCTAGTAG	1928
QY	2113	TCATCAACAGNAGGATTCAGGCAATTACCTCTGCGCATGCGGTGGAAATCGGTTTCATACA	2172
DB	1929	TCATCAACAGNAGGATTCAGGCAATTACCTCTGCGCATGCGGTGGAAATCGGTTTCATACA	1988
QY	2173	AACCTCTTTTAAAGTAAACCCCTGGAAGTCATTGTACACAGACGATTTGGAAGAACTTCTTCA	2232
DB	1989	AACCTCTTTTAAAGTAAACCCCTGGAAGTCATTGTACACAGACGATTTGGAAGAACTTCTTCA	2048
QY	2233	TAAAGATGATGATGGAGATGGCTCTAAGA CAAAGAAATCTCCAATAGCATGACACCTAG	2292
DB	2049	TAAAGATGATGATGGAGATGGCTCTAAGA CAAAGAAATCTCCAATAGCATGACACCTAG	2108
QY	2293	CCAGAAGCTCTGGTACAGAGACCTTCATGACAGCTTCATCAACCCCACTTCTCAACACGAT	2352
DB	2109	CCAGAAGCTCTGGTACAGAGACCTTCATGACAGCTTCATCAACCCCACTTCTCAACACGAT	2168
QY	2353	GGATGATCTCTGTGAACAAGTTTGGAAAAGGGACCGAAAAACAACGTCGGCAAGGCCAGG	2412
DB	2169	GGATGATCTCTGTGAACAAGTTTGGAAAAGGGACCGAAAAACAACGTCGGCAAGGCCAGG	2228
QY	2413	ACATACCCAGGGAAACAGTAAACAAATGGAGACATTTACAAGAAAATAAGAAAGGTAGAAA	2472
DB	2229	ACATACCCAGGGAAACAGTAAACAAATGGAGACATTTACAAGAAAATAAGAAAGGTAGAAA	2288
QY	2473	CAGGAGGACCCACGAATTTGAGAGGGCACCCAGGAGTGTCTGAGCTGCATTAACCTCTAGA	2532
DB	2289	CAGGAGGACCCACGAATTTGAGAGGGCACCCAGGAGTGTCTGAGCTGCATTAACCTCTAGA	2348
QY	2533	AACTCAACAACTAGAAAATTCGCTAGACATAAATCTGGAAAAACAAATGCAATATACAT	2592
DB	2349	AACTCAACAACTAGAAAATTCGCTAGACATAAATCTGGAAAAACAAATGCAATATACAT	2408
QY	2593	GAACTTTTTTCACTGGCAATATGTGGATGTTTTCAATGGTGGGAAATTCAGCTGAGTTCCA	2652
DB	2409	GAACTTTTTTCACTGGCAATATGTGGATGTTTTCAATGGTGGGAAATTCAGCTGAGTTCCA	2468
QY	2653	CCAAATATAAATTAATCCAGTAGTAACCTTCTCTAATAGGCTTTTTTTCC	2702
DB	2469	CCAAATATAAATTAATCCAGTAGTAACCTTCTCTAATAGGCTTTTTTTTC	2518

RESULT 5

US-10-067-632-53
; Sequence 53, Application US/10067632
; Publication No. US20030166849A1
; GENERAL INFORMATION;

APPLICANT: Goodman, Corey S.
Kolodkin, Alex L.
Matthes, David
Bentley, David R.
O'Connor, Timothy

O'Connor, Timothy
 TITLE OF INVENTION: The Semaphorin Gene Family
 NUMBER OF SEQUENCES: 100
 CORRESPONDENCE ADDRESS:
 ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP
 STREET: 268 Bush Street, Suite 3200
 CITY: San Francisco
 STATE: CA

COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Pacentrin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/067,632
FILING DATE: 04-Feb-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/060,610
FILING DATE: <Unknown>
APPLICATION NUMBER: 08/835,268
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415) 343-4342
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 53:
SEQUENCE CHARACTERISTICS:
LENGTH: 2601 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 16..2331
SEQUENCE DESCRIPTION: SEQ ID NO: 53:
US-10-067-632-53

QY 673 GAACCTCACATTTTGAACCGCCGTTGGAGAGTCCATATGACCTTAAGCTCTGACAGC 732
 Db 489 GAACTCACATTTTGAACCGCCGTTGGAGAGTCCATATGACCTTAAGCTCTGACAGC 548
 QY 733 ATCCCTTTTATAGATGGAGATTTATCTCTGGAATGAGTGGTGGGAGGAG 792
 Db 549 ATCCCTTTTATAGATGGAGATTTATCTCTGGAATGAGTGGTGGGAGGAG 608
 QY 793 CTCTGCTACTCTCCGACTCTCTGGGACACCAACCAATCAGACAGACGACATGATC 852
 Db 609 CTCTGCTACTCTCCGACTCTCTGGGACACCAACCAATCAGACAGACGACATGATC 668
 QY 853 CAGGTGGCTCAATGATCCAAAGTTCTATTAGTGGCCCACTCTCAGAGAGTGAATCC 912
 Db 669 CAGGTGGCTCAATGATCCAAAGTTCTATTAGTGGCCCACTCTCAGAGAGTGAATCC 728
 QY 913 TGAAGATGACAAAGTATCTTTCTCTCGTGAATGCAATAGATGGAGAACACTCTGG 972
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 QY 973 AAAAGCTACTCAGCTAGATAGTGTGATATGCAAGATGATCTTGGAGGCGACAGAG 1032
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 QY 1033 TCTGGTGAATTAATGGAACAATCTCTCAAGCTCGTCTGATTTGCTCAGTGCAGGTGCC 1092
 Db 849 TCTGGTGAATTAATGGAACAATCTCTCAAGCTCGTCTGATTTGCTCAGTGCAGGTGCC 908
 QY 1093 AAATGGCATGACACTCAATTTGATGAATGCAAGTGTGATTTCTTAATGAACTTTAAAGA 1152
 Db 909 AAATGGCATGACACTCAATTTGATGAATGCAAGTGTGATTTCTTAATGAACTTTAAAGA 968
 QY 1153 TCCTAAATATCCAGTTGATATGAGTGTGATGATGCACTTCCAGTAACTTTCAAGGATC 1212
 Db 969 TCCTAAATATCCAGTTGATATGAGTGTGATGATGCACTTCCAGTAACTTTCAAGGATC 1028
 QY 1213 AGCCGTGTGATGTATAGCATGATGTGAGAGGGTGTCTTGTGTCATATGCCCA 1272
 Db 1029 AGCCGTGTGATGTATAGCATGATGTGAGAGGGTGTCTTGTGTCATATGCCCA 1088
 QY 1273 CAGGATGGACCCAACTATCAATGAGTGTGATGATGCAAGAGTGTCCCTATCCAGGCC 1332
 Db 1089 CAGGATGGACCCAACTATCAATGAGTGTGATGATGCAAGAGTGTCCCTATCCAGGCC 1148
 QY 1333 AGGAACCTGTCCAGCAAAACATTTGGTGTGTTGACTCTCAAGAGGACCTTCTGTATGA 1392
 Db 1149 AGGAACCTGTCCAGCAAAACATTTGGTGTGTTGACTCTCAAGAGGACCTTCTGTATGA 1208
 QY 1393 TGTTATTAACCTTTGCAAGAGTGTATCAGCATGTATCAATCAGTGTGTTCTATGACAA 1452
 Db 1209 TGTTATTAACCTTTGCAAGAGTGTATCAGCATGTATCAATCAGTGTGTTCTATGACAA 1268
 QY 1453 TCGCCCAATAGTGTATCAAAACCGATGTAAATTTATCAAAATTTGCTAGACCG 1512
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 Db 1389 TCTTAAAGTATGTTCAATTTCTTAAGGAGACTTGGTATGATTTAGAGAGGTTCTGCTGGA 1448
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 Db 1449 AGAATGACAGATTTTTCGGGACCGGCTGATTTTTCAGCAATGGAGCTTCCCTAGACA 1508
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 Db 1509 GCAACAACTATATTTGTTTCAACCGCTGGGTTGCCAGTGTCCCTTTTACACCGGTGGA 1568
 QY 1753 TATTTACGGGAGGAGCGTGTGCTGAGTGTGCTCGCTCGCCCGAGACCTTTACTGTGCTGGGA 1812

Db 1569 TATTTACGGGAGGAGCGTGTGCTGAGTGTGCTCGCCGAGACCTTTACTGTGCTTGGGA 1628
 QY 1813 TGGTTCTCATGTTCTCCCTATTTTCCACTGCAAGAGAGCGCACAGAGCAAGATAT 1872
 Db 1629 TGGTTCTCATGTTCTCCCTATTTTCCACTGCAAGAGAGCGCACAGAGCAAGATAT 1688
 QY 1873 AAGAAATGAGAGCCCACTGACTCTCTGTTCAGACTTACCATGATAATCACCATGGCCA 1932
 Db 1689 AAGAAATGAGAGCCCACTGACTCTCTGTTCAGACTTACCATGATAATCACCATGGCCA 1748
 QY 1933 CAGCCCTGAGAGAGCAATCATCTATGTTAGAGAAATAGTAGCACATTTTGGAAATGCGAG 1992
 Db 1749 CAGCCCTGAGAGAGCAATCATCTATGTTAGAGAAATAGTAGCACATTTTGGAAATGCGAG 1808
 QY 1993 TCCGAAGTCCGAGAGAGCGCTGTCTATTGGCAATTCAGAGGCGAAATGAAGAGCGAAA 2052
 Db 1809 TCCGAAGTCCGAGAGAGCGCTGTCTATTGGCAATTCAGAGGCGAAATGAAGAGCGAAA 1868
 QY 2053 AGAAGAGATCAGAGTGGAGTATCATATCATCAGACAGATCAAGGCTTCTGCTACGTAG 2112
 Db 1869 AGAAGAGATCAGAGTGGAGTATCATATCATCAGACAGATCAAGGCTTCTGCTACGTAG 1928
 QY 2113 TCTACACAGAGAGTTCAGGCAATTAACCTCTGCGATGCGGTGGAAACATGGGTTCATACA 2172
 Db 1929 TCTACACAGAGAGTTCAGGCAATTAACCTCTGCGATGCGGTGGAAACATGGGTTCATACA 1988
 QY 2173 AACTCTTCTTAAGGTAAACCTTGAAGTCAATGACACAGATTTTGGAAAGACTTCTTCA 2232
 Db 1989 AACTCTTCTTAAGGTAAACCTTGAAGTCAATGACACAGATTTTGGAAAGACTTCTTCA 2048
 QY 2233 TAAAGATGATGAGAGATGCTCTTAAGACCAAGAAATGTCCAAATAGCATGACACCTAG 2292
 Db 2049 TAAAGATGATGAGAGATGCTCTTAAGACCAAGAAATGTCCAAATAGCATGACACCTAG 2108
 QY 2293 CCAGAGAGTCTGGTACAGAGACTTCAATGACACTTCAACACCCCAATCTCAACACGAT 2352
 Db 2109 CCAGAGAGTCTGGTACAGAGACTTCAATGACACTTCAACACCCCAATCTCAACACGAT 2168
 QY 2353 GGATGAGTCTGTGAACAGTGTGGAAAGGAGCCGAAACACAGCTCGGCAAGGCCAGG 2412
 Db 2169 GGATGAGTCTGTGAACAGTGTGGAAAGGAGCCGAAACACAGCTCGGCAAGGCCAGG 2228
 QY 2413 ACATACCCCGAGGAGCAAGTAAACAAATGGAAGCACTTACAGAAATAAAGAAAGGTAGAAA 2472
 Db 2229 ACATACCCCGAGGAGCAAGTAAACAAATGGAAGCACTTACAGAAATAAAGAAAGGTAGAAA 2288
 QY 2473 CAGGAGGACCCAGCAATTTGAGAGGCGACCCAGAGTGTCTGAGCTGCATTAACCTTAGA 2532
 Db 2289 CAGGAGGACCCAGCAATTTGAGAGGCGACCCAGAGTGTCTGAGCTGCATTAACCTTAGA 2348
 QY 2533 AACCTCAACAAAGTAGAAAATTCCTAGACAAATAAATGGAAGAAACAAATGCAATATACAT 2592
 Db 2349 AACCTCAACAAAGTAGAAAATTCCTAGACAAATAAATGGAAGAAACAAATGCAATATACAT 2408
 QY 2593 GAACTTTTTCATGCGCAATTTGAGTGTGTTTCAATGTTGGGAAATTCAGCTGAGTTCCA 2652
 Db 2409 GAACTTTTTCATGCGCAATTTGAGTGTGTTTCAATGTTGGGAAATTCAGCTGAGTTCCA 2468
 QY 2653 CCAATTATAAATTAATCCATGAGTAACTTTCCTAATAGGCTTTTTTTC 2702
 Db 2469 CCAATTATAAATTAATCCATGAGTAACTTTCCTAATAGGCTTTTTTTC 2518

RESULT 6

US-10-404-438-2
 ; Sequence 2, Application US/1040438
 ; Publication No. US2003023411A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ono Pharmaceutical Co., Ltd.
 ; TITLE OF INVENTION: NOVEL POLYPEPTIDE, cDNA ENCODING THE SAME, AND USE THEREOF
 ; FILE REFERENCE: Q59878
 ; CURRENT APPLICATION NUMBER: US/10/404,438

; CURRENT FILING DATE: 2003-04-02
; PRIOR APPLICATION NUMBER: US/09/582,419A
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: PCT/JP98/05952
; PRIOR FILING DATE: 1998-12-25
; PRIOR APPLICATION NUMBER: P. Hei. 9-358811
; PRIOR FILING DATE: 1997-12-26
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 2
; LENGTH: 2331
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-10-404-438-2

Query Watch 26.5%; Score 718.6; DB 16; Length 2331;
Best Local Similarity 61.9%; Pred. No. 5e-206;
Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;
QY 269 AATGGGAAGACAAATCTGCCAGGCTGAAATATCTTACAAAGAAATGTTGAAATCCAAAC 328
Db 109 ACTTTGAACAAATATCTCAAGACTCAAGCTAACTCAAAAGACTTGTCTCTTCAAAAT 168
QY 329 AATGTGATCACTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATACACCTTCCCTTTGGAT 388
Db 169 AGCTGTATCCCTTTTGGGTTTCATCAGAAGACTGGATTTCAAACCTTCTCTTAGAT 228
QY 389 GAGGAACGAGTAGCTGTATGTTGGAGCAAGAGATCATAATTTTCATTTGACCTGGTT 448
Db 229 GAGGAAGAGGAGGAGCTGTCTTGGAGCCAAAGACCACATCTTTCTACTCAGTCTGGTT 288
QY 449 AA---TATCAAGGATTTTCAAAGATTTGTGGCCAGATCTTTACACCAGAAGATGAA 505
Db 289 GACTTAACAAAAATTTAAGAGATTTATGGCTGTGCAAGAGAGGTTGGAATTA 348
QY 506 TGCAGTGGCTGGAAAAGACATCTCGAAGAAATGTCTAAATTTTCATCAAGTACTTAAG 565
Db 349 TGTAAATAGCTGGGAAGATGCCAATACAGAAATGTGCAAAATTTTCATCAGAGTACTTCAG 408
QY 566 GCATATAATCAGACTCACTGTACGCTGTGAACGGGGCTTTTCATCCATTTGACCC 625
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QY 626 TACATTTGAATTTGGACATCATCTCTGAGGACATATTTTAAAGCTGGAGAACTCAATTTT 685
Db 469 TATATTGATCTTGGAGCTTACAAGGAGGATATTAATTCAACTAGACACACGTAATTG 528
QY 686 GAAAAGCGCGTGGGAAGAGTCCATATGACCTTAAGCTGTGACAGCATTCCTTTTAAATA 745
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QY 746 GATGGAGAAATTAATCTCTGGAATCTGAGTGAATTTTATGGGCGAGACTTTTGTCTATCTC 805
Db 589 GATGAGTACCTTACTCTGGAACAGCTTCTGATTTCTTCTTGGCAAGATACCTGATCTACT 648
QY 806 CGAATCTTTGGGC-----ACCACACCAATTCAGACAGAGCAGCATGATTCACGG 856
Db 649 CGATCCCTTTGGCCCTTACTCATGACCACCACTACATCAGAACTGACATTTTCAGAGCACTAC 708
QY 857 TGGCTCAATGATCCAAAGTTCAATAGTCCCACTCATCTCAGAGAGTGAATCCCTGAA 916
Db 709 TGGCTCAATGAGCAAAATTTATGGAATCTTTTCACTTACCAGACACCTCAATCCAGAT 768
QY 917 GATGCAAAAGTACTTTTCTTCGTTGAAAATGCAATAGATGGAGAACACTCTGGAAAA 976
Db 769 GATGATAAAATATAATTTCTTCTTCTGTAATCATCTCAAGAGGAGCAGTACCTCCGATAAA 828
QY 977 GCTACTCAGCTAGAAATAGTCAATATGCAAGATGACTTTGAGGGCAAGAGTCTG 1036
Db 829 ACCATCTTTCTCGAGTTGGAAGAGTTTGTGAAGATGATGTAGGAGGACAAACGAGCGCTG 888
QY 1037 GTGAATAAATGGAACAATCTCTCAAAGCTGTCTGATTTTGTCTCAGTCCAGGTCCTCAAAAT 1096

Db 889 ATAAACAAGTGGACGACCTTTTCTTAAGGCCACGACTGATTTGCTCAATTTCTGGAAGTAT 948
QY 1097 GGCATTGACACTCAATTTTGATGACCTGAGATGATATTCCTAATGAATTTAAAGTCCCT 1156
Db 949 GGGCAGATCTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCAACAGAGATGAA 1008
QY 1157 AAAAAATCCAGTTGTATATGGAGTGTTCAGACTTCCAGTAACATTTTCAAGGGATCAGCC 1216
Db 1009 AGAAATCCTGTAGTATATGGAGTCTTTACTACAACAGCTCCATCTTTCAAAGGCTCTGCT 1068
QY 1217 GTGTGTATGATAGCATGATGATGAGAGGGTGTCTTGTGTCATATGCCACAGG 1276
Db 1069 GTTTGTGTATAGCATGGCTGACATCAGAGCAGTTTTTAATGTCCTATGTCATTAAG 1128
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Db 1129 GAAAGTGCAGACCATCTGTTGGTGCAGTATGATGGGAGAAATTCCTTATCCACGSCCTGGT 1188
QY 1337 ACTTGTCCCAAGCAAAACATTTG---GTGTTTTGACTCTACAAGAGACCTTCTCTGATGAT 1393
Db 1189 ACATGTCCCAAGCAAAACCTATGACCCCACTGATTAAGTCCACCCAGATTTTCCAGATGAT 1248
QY 1394 GTTATAACCTTTGCAAGAAGTCTCCAGCCATGTACAATCCAGTGTTCCTATCAACAAT 1453
Db 1249 GTCATCAGTTTCATAAAGCGCACTCTGTGATGTATANGTCGTATACCCAGTTGACGA 1308
QY 1454 CGCCCAATAGTGTCAAAACGGATGTAATTAATCAATTTACAAATTTGTCGTAGACGA 1513
Db 1309 GGACCAACGTTCAAGAGATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCAT 1368
QY 1514 GTGATCCAGAAGATGACAGATGATGTATGTATTTATCGGAACAGATTTGGGACCGTT 1573
Db 1369 GTCATTCAGAGAGTGGCCAGTACGATGATTAATGTTCTTGGAAACAGACATTTGGAACGTG 1428
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Db 1429 CTCAAAGTTGTACGATTTCAAAGGAAAAGTGG---AATATGGAAGAGGTAGTGTGGAG 1485
QY 1634 GAAATGACAGCTTTTCGGGAACCGACTGTCTATTTACAGATGAGCTTTTCCATTAAGCAG 1693
Db 1486 GAGTTGCAGATATTCAGACACTCATCAATCATCTTGAACATGGAATTTGTCTCTGGAAGCAG 1545
QY 1694 CAACAACTATATTTGTTTCAACGGTGGGGTTGCCAGCTCCCTTTTACACCGGTGTGAT 1753
Db 1546 CAACATTTGATCTGTTCCCGAGATGATTAAGTTAGTTCAGCTCTCTTTCACACATGGCAG 1605
QY 1754 ATTTACGGGAAAGCGTGTGCTGATGTGTGCTCCCGAGACCCCTTACTGTGTGGGAT 1813
Db 1606 ACTTATGGGAAAGCTTTGCGCAGACTGTGTCTTTGCCAGAGACCCCTTACTGTGCTGGAT 1665
QY 1814 GGTCTGTCATGTTCTCGCTATTTTCCACTGCAAGAGAGCGCAACAGACGACAGATATA 1873
Db 1666 GGAATGCACTCTCTCGATATGCTCTACTTTCTAAAGAGAGAGCTAGACGCCAAGATGTA 1725
QY 1874 AGAAATGGAGACCCACTGACTCTACTGTCAGACTTACCACTGATTAATCAATCAATGCCAC 1933
Db 1726 AATATATGGCACCCCAATCACCCAGTGTGGGACATCGAAGACAGCATTAAGTCAATG--AA 1782
QY 1934 AGCCCTGGAAGAGAGATCATCTATGTTGAGAGATGATGAGACATTTTGGNATCGAGT 1993
Db 1783 ACTGCTGATGAAAAGGTGATTTTGGCATTTGAATTTAACTCAACCTTTCTGGAATGTATA 1842
QY 1994 CCGAAGTCGAGAGAGCGGTGTTCTATTGGCAATTCAGAGCGGGAATGAAGAGCGAAAA 2053
Db 1843 CCTAATCCCAACGAACACTATTAATGGTATATCCAGAGGTTCAGGGGATGAGCATCGA 1902
QY 2054 GAAGAGATCAGATGATGATCATATCATCAGAGACAGATCAAGCCCTTCTGCTACCTAGT 2113
Db 1903 GAGGAGTTGAAGCCCGATGAAGAATCATCAAAACGGAATATGGGCTACTGATTCGAAAT 1962
QY 2114 CTCAACAGAGGATTTGAGCAATTAACCTCTGCTGATGCGGTGGAACATGGGTTTCAACAA 2173
Db 1963 TTGCAAGAGAGGATTTCTGGGATGATTAATGCAAGAGCCAGGAGCAGCACTTTTCAATCCAC 2022

OY 2174 ACTCTTCTTAAGTAACCTGGAAGTCATTGACACAGAGCATTGGAAGAACTTCTTCAT 2233
Db ACCATAGTGAAGCTGACTTTGATGTCTTGAATGTGATGAAATGACATGGAATAATACCCAGAGG 2082
OY 2234 AAAGATGATGATG 2246
Db 2083 GCAGAGCATGAGG 2095

RESULT 7

US-09-946-374-309
; Sequence 309, Application US/09946374
; Publication No. US20030073129A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Pacini, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Smith, Victoria
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1
; CURRENT APPLICATION NUMBER: US/09/946,374
; PRIOR FILING DATE: 2001-09-04
; PRIOR APPLICATION NUMBER: 60/098716
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098723
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098749
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098750
; PRIOR FILING DATE: 1998-09-01
; PRIOR APPLICATION NUMBER: 60/098803
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098821
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098843
; PRIOR FILING DATE: 1998-09-02
; PRIOR APPLICATION NUMBER: 60/098836
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/098596
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/098598
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/098602
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/098642
; PRIOR FILING DATE: 1998-09-09
; PRIOR APPLICATION NUMBER: 60/098741
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/098754
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/098763
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/098792
; PRIOR FILING DATE: 1998-09-10

; PRIOR APPLICATION NUMBER: 60/099808
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099812
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099815
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/099816
; PRIOR FILING DATE: 1998-09-10
; PRIOR APPLICATION NUMBER: 60/100385
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100388
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100390
; PRIOR FILING DATE: 1998-09-15
; PRIOR APPLICATION NUMBER: 60/100584
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100627
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100661
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100662
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100664
; PRIOR FILING DATE: 1998-09-16
; PRIOR APPLICATION NUMBER: 60/100683
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100684
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100710
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100711
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100848
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100849
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/100919
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/100930
; PRIOR FILING DATE: 1998-09-17
; PRIOR APPLICATION NUMBER: 60/101014
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101068
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101071
; PRIOR FILING DATE: 1998-09-18
; PRIOR APPLICATION NUMBER: 60/101279
; PRIOR FILING DATE: 1998-09-22
; PRIOR APPLICATION NUMBER: 60/101471
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101472
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101474
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101475
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101476
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101477
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101479
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: 60/101738
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101741
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101743
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101915
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/101916
; PRIOR FILING DATE: 1998-09-24
; PRIOR APPLICATION NUMBER: 60/102207

[illegible]

QY	1394	GTTATAACCTTTGCGAAGAAGTCATCCAGCCATGTACAATCCAGTGTTCCTCATGAACAAT	1453
Db	1355	GTCAATCAGTTTTCAAAAAGCGGCACCTCTGTGATGTATAAGTCCGTATACCCTAGTTTGCAAG	1414
QY	1454	CGCCCAAATAGTAGATCAAAACGGATGTAATATTCAATTTACAAATTTGCTGTAGACGA	1513
Db	1415	GGACCAACGTTCAAGAGNAATCAATGTGGATACAGACTGACACAGATAGTGGTGGATCAT	1474
QY	1514	GTGGATCGAGAAGATGGAAGATGATGTATGTTTATCGGAACAGATGTTGGGACCGTT	1573
Db	1475	GTCAATTGCAAGAAGATGGCCAGTAGCATGTAACTTTCTTTGGAACACAGACATTGGAACTGTC	1534
QY	1574	CTTAAAGTAGTTTCAATTCCTPAAGSGACACTTGGTATGATTTTGAAGAGAGTCTGCTCGAA	1633
Db	1535	CTCAAGTTGTACGCAATTCBAAGGAANAAGTGG---AATATGGAAGAGGTAGTCTGGAG	1591
QY	1634	GAAATGACAGTTTTTCGGAAACGAGTCGTATTTCAGCAATGGAGCTTTCACCTAAGCAG	1693
Db	1592	GAGTTGCGAGATATTCAAAGCACATCATCAATCATCTCGAACATGGAAATGTCTCTGAAGCAG	1651
QY	1694	CAACAACATATATTGTTTCAACGGCTGGGGTTGCCACGCTCCCTTTACCGCGTGTGTAT	1753
Db	1652	CAACAAATGTACATTGGTCCCAGATGGATTAGTTTCACTCTCCTTCGACAGATGGCAC	1711
QY	1754	ATTTACGGGAAGCGTGTGTGATGTGCTCGCCGAGACCCCTACTGTGCTTGGGAT	1813
Db	1712	ACTTATGGGAAGCTTGGCAGACTGTGTGCTTGGCAGAGACCCCTACTGTGCTCGCTGGGAT	1771
QY	1814	GGTCTGTCATGTTCTCCGATATTTTCCACATGCAAGAGACGCAAGAGACGAAGAATATA	1873
Db	1772	GGAAATGCATGCTCTCGAATGCTCTACTTTCTPAAAGGAGAGCTAGAGCCCAAGATGTA	1831
QY	1874	AGAAATGGAGACCCACTGACTCTACTGTTCAGACTTACCATGATAATCACCATTGGCCAC	1933
Db	1832	AAATATGCGGACCAATCACCAGCTGCTGGGACATCGAAGACGCAATTAGTCATG---AA	1888
QY	1934	ASCCCTGAAGAGAGAAATCATCTATGGTGTAGAGANTAGTAGCACATTTTTCGGAATGCAGT	1993
Db	1889	ACTGCTGATGAAGAAGGTGATTTTGGCATTTGAATTTACTCAACCTTCTCGAATGTATA	1948
QY	1994	CCGAAGTCCGAGAGAGCGCTGGTCTATTTGGCAATTCAGAGCGGAANTGAAGACGAAAA	2053
Db	1949	CCTAAATCCCAACAAGCAACTATTAAATGGTATATCCAGAGGTCAAGGGGATGAGCATCGA	2008
QY	2054	GAAGAGATCAGATGCGATGATCATATCATCAGACACAGATCAGAGCCCTTCTGCTACGTAGT	2113
Db	2009	GAGGAGTTGAAGCCGATGAAGAATCATCAAAACGGAATATGGGCTACTGATTCGAAGT	2068
QY	2114	CTACAACAAGAGGATTCAGGCAATTAACCTTGCCATGGCGTGGAAATGGGTTTCATCAA	2173
Db	2069	TTGCAGAAGAAGGATCTGGGATGTATTAATGCAAGCCAGGAGCACACTTTTCATCCAC	2128
QY	2174	ACTCTTCTTAAGTAAACCTCGGAGTCNTTGAACACAGACATTTTGGAGAGACTTCTTCAT	2233
Db	2129	ACCATAGTGAAGCTGACCTTTGAATGTCATTGGAAATGAACAGATGGAAATATCCACAGG	2188
QY	2234	AAAGATGATGATG 2246	
Db	2189	GCAGAGCATGAGG *2201	

RESULT 8

US-100-015-395A-309
; Sequence 309, Application US/10015395A
; Publication No. US20040073015A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman

QY 977 GCTACTCAGCTAGATAGTCTAGATATGCAAGATGACTTTGGAGGGCACAGAAGTCTG 1036
 Db 935 ACCATCTCTCTCGAGTGGAGAGGTTTGTAGAAATGATAGTAGGAGCAACGCGAGCTG 994
 QY 1037 GTCAATAAATGGACACATCTCCTCAAGAGTCTGCTGATTTGCTGCTGAGTCCAGGTCAGAT 1096
 Db 995 ATAAACAAGTGGACGACTTTCTTAAAGGCGAGACTGATTTGCTCAATCTCTGGAAGTGAT 1054
 QY 1097 GGCATTGACACTCATTTTATGATGAATGCGAGGATGATCTCTAATGAATTTTAAAGATCT 1156
 Db 1055 GGGCGAGATATCTTCTGATGAGCTTCAAGATATTTATTTACTCCCAACAGAGTAA 1114
 QY 1157 AAAATCCAGTTGTATATGAGAGTGTATGAGCTTCCAGCTTCCAGTAAATTTTCAAGGATCAGCC 1216
 Db 1115 AGAAATCCTGTATATATGAGTCTTCTTAAAGGCGAGACTGATTTGCTCAATCTCTGGAAGTGAT 1174
 QY 1217 GTGTGATGTATAGCATGATGATGAGAGGTTCTCTTGGTCCATATGCCACAGG 1276
 Db 1175 GTTTGTGTATAGCATGCTGATGATGAGAGGTTCTTAAAGGCGAGACTGATTTGCTCAATCTCTGGAAGTGAT 1234
 QY 1277 GATGGACCAACTATCAATGGGTGCTTATCAAGGAAGTCCCTTATCCAGGCGCAGGA 1336
 Db 1235 GAAAGTGCAGACCATCGTTGGGTGCGATGATGAGAGGATTTCTTATCCAGGCGCTGT 1294
 QY 1337 ACTGTGCCAGCAACATTTG---GTGGTTTGTACTCTACAAAGGACCTTCTCTGATGAT 1393
 Db 1295 ACATGTCCAGCAACCTATGACCATCTGATTAAGTCCACCGAGATTTTCCAGATGAT 1354
 QY 1394 GTTATAACCTTTGCAAGAGTCTATCCAGCATGTATCAATCCAGTGTCTTCTATGAACAAT 1453
 Db 1355 GTCATCAGTTTCATAAAGCGGACCTGCTGATGATATAGTCCGTATATCCAGTTCGAGGA 1414
 QY 1454 CCGCCCAATAGTATCAAAAGGATGTAAATATCAATTTACAAATTTGTGTAGACGGA 1513
 Db 1415 GGACCAAGCTTCAAGAGATCAATGTGGATTACAGACTGACACAGATAGTGTGTATCAT 1474
 QY 1514 GTGGATGCAAGAGATGAGCATGATGATGATTTATCGGAACAGATGTTGGGACCGTT 1573
 Db 1475 GTCAITGCAAGATGCGCAGTACGATGTAATGTTTCTTGGACAGATTTGGAATGTC 1534
 QY 1574 CTTAAAGTATTTCAATCTTAAAGGAGCTTGGTATGATTTAGAAAGGTTCTGTGCGAA 1633
 Db 1535 CTCAAAGTTGTGAGCATTTCAAAGGAAAAGTGG---AATATGGAAGAGGTAGTGTGGAG 1591
 QY 1634 GAAATGACATTTTTCGGGACCGACTGCTATTTTTCAGCAATGAGCTTTCACCTAAGCAG 1693
 Db 1592 GAGTTGCAATATCAAGCATCTATCAATCATCTTTGAACATGGAATGCTCTCTGAAGCAG 1651
 QY 1694 CAACAACTATATATTTGGTTCAACGGCTGGGGTTGCCAGCTCCCTTTACACGGGTGTGAT 1753
 Db 1652 CAACAAATGTACATTTGGTTCCGAGATGATGATTTAGTTTCACTCTCTCTTCCAGATGCGAC 1711
 QY 1754 ATTTACGGGAAGCTGTGTGAGTTGCTCGCCCGAGACCTTACTGTGCTTGGAT 1813
 Db 1712 ACTTATGGAAGCTTGGCGAGACTGTTGCTCTGCGAGACCCCTACTGTGCTGCGAT 1771
 QY 1814 GGTCTGCTATGTTCTGCTATTTTCCCACTGCAAGAGACGCAACAAAGACGACAGATATA 1873
 Db 1772 GGAATGATGCTCTGATATGCTCTTACTTCTTAAAGGAGAGTACAGCGCAAGATGTA 1831
 QY 1874 AGAATGAGACCCACTGACTGCTGTTGCTGAGCTTACACATGATATACCATGGCCAC 1933
 Db 1832 AAATATGCGACCAATCACCCAGTGTGGGACATCGAAGACAGCATTAGTTCATG---AA 1888
 QY 1934 AGCCCTGAAGAGAGATCATCTATGTTGTAGAGATAGTACCATTTTGGATGAGT 1993
 Db 1889 ACTGCTGATGAAGGATGATTTTGGCAATGAAATTTAACTCAACCTTCTGGAATGATA 1948
 QY 1994 CCGAAGTCCGAGAGGCGCTGCTTATTTGGCAATTTCCAGAGCGCAAAATGAAGACGCAAAA 2053
 Db 1949 CCTAAATCCCAACAGCAACTATTAAATGGTATATCCAGAGGTGAGGGGATGACATCGA 2008
 QY 2054 GAAGATCAGAGTGGATGATCATCATCAGGACAGATCAAGGCTTCTGTACGTAGT 2113

Db 2009 GAGAGTTGAGCCCGATGAAGATCATCAAAACGGAATATGGCTACTGATTCGAAGT 2068
 QY 2114 CTACAAACAAGAGGATTCAGCAATTAACCTCTGCCATCGGTGGAAACATGGTTCATACAA 2173
 Db 2069 TTGAGAAGAAGAGTCTTGGGATGATTAATCTGCAAAAGCCAGGAGCACATTTTCATCCAC 2128
 QY 2174 ACTCTTCTTAAAGTAAACCTTGGAGTCTATTTGACACAGAGCATTTGGGAAGACTTCTTCAT 2233
 Db 2129 ACCATAGTGAAGCTGATCTTTGAATGTCTTGAAGATGAACAGATGGAATAATACCCAGG 2188
 QY 2234 AAAGATGATGATG 2246
 Db 2189 GCAGAGATGAGG 2201

RESULT 9
 US-10-206-915-347
 ; Sequence 347, Application US/10206915
 ; Publication No. US20040029221A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; FILE REFERENCE: P3430R1C513
 ; CURRENT APPLICATION NUMBER: US/10/206,915
 ; CURRENT FILING DATE: 2002-07-26
 ; PRIOR APPLICATION NUMBER: 10/052586
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059266
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063120
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063121
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063486
 ; PRIOR FILING DATE: 1997-10-21
 ; PRIOR APPLICATION NUMBER: 60/063540
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063541
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063544
 ; PRIOR FILING DATE: 1997-10-28
 ; Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 347
 ; LENGTH: 3871
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-10-206-915-347

Query Match 26.5%; Score 718.6; DB 13; Length 3871;
 Best Local Similarity 61.9%; Pred. No. 7.4e-206;
 Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;
 QY 269 ATGGGAAGAAACAATGTCACAGGCTGAATTTATCTCAAAAGAAATGTTGGAATCCAAAC 328
 Db 215 ACTTTGAAGAAATATTCAGAGCTCAAGCTCAAGAGTGTCTGCTTTCAAT 274

QY 329 AATGTGATCACTTTCAATGCTTGGCCAAACAGCTCCAGTTATCATACACTTCTCTTTGGAT 388
Db 275 AGCTGTAATCCCTTTTGGTTCATCAGAGAGACTGGATTTTCAAACCTCTCTTAGAT 334
QY 389 GAGAAACCGAGTAGCTGTATGTGGAGCAAAAGGATCACAATTTTCAATTCGACCTGGTT 448
Db 335 GAGAAACAGAGCGAGCTGCTTTGGGAGCAAAAGACCAATCTTTCTACTCAGTCTGGTT 394
QY 449 AA---TATCAAGATTTTCAAPAGATTTGTGSCCAGTATCTTACACAGAGAGATGAA 505
Db 395 GACTTAAACAAAATTTTAAAGATTTTATGGCCTGTGCAAGAAAGCGGTGAATTA 454
QY 506 TGAAGTGGCTGGAAAGACATCTTGAAGAAATGTGCTAAATTTTCAATCAAGGTACTTAAG 565
Db 455 TGTAAATAGCTGGGAAAGATGCAATACAGAGATGTGCAAAATTTTCAATCAGAGTACTTCAG 514
QY 566 GCATATAATCAGACTCACTTTGACGCTGTGGAAAGGGGCTTTTCAATCCAAATTTGCACC 625
Db 515 CCTATAACAAAATTTTAAAGATTTTATGGCCTGTGCAAGAAAGCGGTGAATTA 574
QY 626 TACATTAATTTGGAATCATCTGAGCAATATTTTAAAGTGGAGAACTCAATTTT 685
Db 575 TATATTGATCTTGGAGTACAAAGGAGGATATTTATTTCAAACTAGACACACATAATTTG 634
QY 686 GAAACCGGCGTGGGAGAGTCCATATGACCTTAAGCTGCTGACAGCATCTCTTTTAATA 745
Db 635 GAGTCTGGCAGACTGAAATGTCTTTTCGATCTCAGAGCTTTTGTCTTCAATGACA 694
QY 746 GATGGAGAAATTAATCTCTGGAATCTGAGTGAATTTTATGGGCGAGACTTTTGTCTATCTTC 805
Db 695 GATGAGTACCTTACTCTGGAACAGCTTCTGATTTCTTGGCAAGAGTACTGCAATTTG 754
QY 806 CGAATCTTGGGC-----ACCACCAACCAATCAGACAGAGCAGCATGATTTCCAGG 856
Db 755 CGATCCCTTGGGCTACTCATGACCAACCACTACATCAGAACTGCAATTTTCAAGCACTAC 814
QY 857 TGCTCAATGATCCAAAGTTAATAGTGGCCACCTCATCTCAGAGAGTGAACAATCTGAA 916
Db 815 TGCTCAATGAGCAAAATTTATTTGAACTTTCTTCAATACCAAGACACCTCAATCCAGAT 874
QY 917 GATGACAAAGTATATCTTTCTCGTGAATGCAATAGATGGAGAGACATCTTGGAAA 976
Db 875 GATGATTAATATATTTCTTCTTCTGTAATCATCTCAGAGAGGAGTACCTCCGATAA 934
QY 977 GCTACTCACCTAGAAATAGTCAATGCAAGATGATTTTGGAGGCGCAGAAAGTCTG 1036
Db 935 ACCATCTTTCTCGAGTTGGAAGAGTTTGTAAAGATGATGTAGGAGGACAAAGCGAGCTG 994
QY 1037 GTGAATAATGGACAACTTCTCAAGCTCTGATTTGCTCAGTCCAGGTCCTCAAT 1096
Db 995 ATAAACAGTGGAGAGCTTTCTTAAGCCAGACTGATTTGCTCAATTTCTTGGAGTAT 1054
QY 1097 GGCATTTGACACTCAATTTGATGAACTGAGGATGATTTCTTAATGAACTTTTAAAGATCT 1156
Db 1055 GGGGCGATATCTTCTGATGAGCTTCAAGATATTTTACTCTCCCAAGAGATGAA 1114
QY 1157 AAAATCCAGCTGTATATGAGTGTATGAGCTTCCAGTAACTTTTCAAGGAGTACAGCC 1216
Db 1115 AGAATCTGTATATGAGTCTTTTACTTAAACAGCTCATCTTCAAGGCTCTGCT 1174
QY 1217 GTGTATGATATGAGTATGATGTGAAGGGTGTTCCTTGTGCTCATATGCCCCAGG 1276
Db 1175 GTTGTGTATGATGATGCTGATCAGAGAGGTTTTTAAATGTTGCTCATATGCTCATAG 1234
QY 1277 GATGGACCCCAATCATCAATGGGTGCTTATCAAGGAGAGTCCCTATCCACGCGCAGGA 1336
Db 1235 GAAAGTGCAGACCATCTTGGGTGCAATGATGAGGAGAAATCTTATCCAGGCTTGGT 1294
QY 1337 ACTTGTCCAGCAAAACATTTG---GTGGTTTGTACTCTCAAGAGACCTTCTCTGATGAT 1393
Db 1295 ACATGTCCAGCAAAACCTATGACCACTGATTAAGTCCACCGAGATTTTCCAGATGAT 1354
QY 1394 GTTATAACCTTTGCAAGAGTCAATCCAGCCATGTACAATCCAGTGTCTTCTATGAACAT 1453

Db 1355 GTCATCAGTTTTCATAAAACGGCACTCTGTGATGTATAGTCCGTATATACCCAGTTGCAGGA 1414
QY 1454 CCCCCAATAGTATCAAAACGGATGTAAATATCAATTTACAAATTTGCTGTAGACCGA 1513
Db 1415 GGACCAACGCTTCAAGAGAAATCAATGTGGATTTACAGATGACACAGATAGTGGTGGATCAT 1474
QY 1514 GTGGATGACAGAGATGGACAGTATGTATGTATTTATCGGAAACAGATGTGGGACCGGT 1573
Db 1475 GTCAATTCAGAGATGGCCAGTACAGTATGTATTTCTTGGAAACAGACATTTGAACTGTC 1534
QY 1574 CTTAAAGTATGTTTCAATTTCTTAAAGAGACTTGGTATGATTTAGAGAGTCTTCTCGGAA 1633
Db 1535 CTCAAAGTGTGACATTTCAAGGAAAGTGG---AATATGGAAGAGGTAGTGTCTGGAG 1591
QY 1634 GAAATGACAGTTTTTCGGGAAACCGACTGCTATTTTTCAGCAATGGAGCTTTTCCACTAAGCAG 1693
Db 1592 GAGTTGCAAGATTTCAAGCACTCATCAATCATCTTGAACATGGAATTTGCTCTGAGGACG 1651
QY 1694 CAAACACTATATTTGTTTCAACGGTGGGGTTCGCCAGTCCCTTTTACACCGGTGTAT 1753
Db 1652 CAACAATGTATTTGTTTCCCGAGATGGATTTAGTTTCACTCTCTTTCACAGATGGCAG 1711
QY 1754 ATTTACGGGAAAGCGTGTGAGTGTTCCTCGCCGAGACCTTTACTTGTCTTGGGAT 1813
Db 1712 ACTTATGGGAAAGCTTTCGACAGCTGTTGCTTCCAGAGACCTTACTGTGCTGGAT 1771
QY 1814 GGTTCGATGTTTCTCGTATTTTCCACTGCAAGAGAGACGACAGACGACAGATATA 1873
Db 1772 GGAATGTATGCTCTCGATATGCTTCTTCTTAAAGGAGAGCTAGACCCCAAGATGA 1831
QY 1874 AGAATGGAGACCCCACTGACTCACTGTTTCAAGCTTACCAATGATATCAATCAATGAGCCAC 1933
Db 1832 AATATGGGACCCCAATCACCAGCTGCTGGACATCGAAGACAGCAATTTACTCATG---AA 1888
QY 1934 AGCCTGAGAGAGAACTCATCTATGTTGTAGAGATAGTAGCACAATTTTGGATGAGT 1993
Db 1889 ACTGCTGATGAAAGGATTTTGGGCAATGAAATTTAACTCAACCTTTCTGGAATGTATA 1948
QY 1994 CCGAAGTCCGAGAGAGCGCTGCTCTATTTGGCAATTTCCAGAGGGGAAATGAAGAGCGAAA 2053
Db 1949 CCTAATCCCAACAGCACTATTTAATGGTATATCCAGAGGTCAGGGATGAGCATCGA 2008
QY 2054 GAAGAGATCAGAGTGGATGATCATCATCAGGACAGATCAAGCCTTCTGCTACGTAGT 2113
Db 2009 GAGGATTTGAAGCCCGATGAAAGAAATCATCAAAACGGAATATGGGCTACTGATTCGAAAT 2068
QY 2114 CTACAACAGAGGATTCAGGCAATTTAGCTCTGCCATCGGTTGGAACATGGGTTTATACAA 2173
Db 2069 TTGCAGAGAGAGGATTTCTGGGATGATTTACTTGCAAGCCCGAGGACACATTTTATCCAC 2128
QY 2174 ACTTCTTTAAGGTAACCTGGAAGTCAATGACAGAGATTTGAGAGTCTTCTTCAT 2233
Db 2129 ACCATAGTGAAGCTGACTTTGAATGTCTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGT 2188
QY 2234 AAAAGATGATGATG 2246
Db 2189 GCAGAGCATGAGG 2201

RESULT 10.

US-10-199-670-347
; Sequence 347, Application US/10199670
; Publication No. US2004003560A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C401
; CURRENT APPLICATION NUMBER: US/10/199,670
; CURRENT FILING DATE: 2002-07-19
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 347
; LENGTH: 3871
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-199-670-347

Query Match 26.5%; Score 718.6; DB 13; Length 3871;
Best Local Similarity 61.9%; Pred. No. 7.4e-206;
Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;

QY 269 AATGGAGAAACAATGTCRAGGCTGAAATATCTCAAGAAATGTTGGAATCCAAAC 328
DB 215 ACTTTGAAGCAAAATATTCAGAGCTCAAGCTAACTCAAGAGCTTCTGCTTTCAAAT 274
QY 329 AATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTATCATACCTTCTCTTTGGAT 388
DB 275 AGCTGTATTCCTTTTGGGTTTCATCAGAGAGCTGGATTTCAAACCTTCTCTTAGAT 334
QY 389 GAGGAACGGAGTAGGCTGTATGTTGGAGCAAGGATCACATATTTTCAATTCGACCTGGTT 448
DB 335 GAGGAAGAGGCGAGCTGCTCTTGGAGCCAAAGACCACATCTTTTCTACTCAGTCTGGTT 394
QY 449 AA---TATCAAGGATTTTCAAAGATTTGTGGCCAGTATCTTACACCAGAGAGATGAA 505
DB 395 GACTTAACAAAAATTTAAGNAGATTTATTGGCTCTGTCGAAGGACGGGTGAATTA 454
QY 506 TCGAAGTGGCTGGAAAGACATCTCGAAGAAATGTCTAAATTTCAACAGGTACTTAAAG 565
DB 455 TGTAAATTAGCTGGGAAAGATGCCAATACAGAAATGTGCAATTTTCAACAGAGTACTTCAG 514
QY 566 GCATATAATCAGACTCACTGTACGCTGTGACGGGGCTTTTCACTCAATTTGCAAC 625
DB 515 CCTTAACAAACTCAATATATGTGTGGAACCTGGAGCATTTCACTCAATATGTGGG 574
QY 626 TACATTGAAATGGACATCTCTGAGGACAAATATTTTAAAGCTGGAGAACTCAATTTT 685
DB 575 TATATTGATCTGGAGTCTCAAGAGGATATTTATTTCAAAGTACAGACATAAATTG 634
QY 686 GAAACGGCCGTGGGAAGTCCATATGACCTTAAGCTGTGACAGCATTCCTTTTAAATA 745
DB 635 GAGTCTGCAGACTGAAATGCTTTTCGATCCTCAGCAGCCTTTTGTCTTCAGTAATGACA 694
QY 746 GATGAGAAATTATATCTCTGGAACCTGCAGCTGATTTTATGGGGCGAGACTTTTGCTATCTC 805

695 GATGAGTACCTCTACTCTGGAAACAGCTTCTGATTTCCTTGGCAAGATACTGCATTCACT 754
806 CGAACTCTTGGGC-----ACCACACCCCATCAGGACAGACAGCATGATTCAGG 856
755 CGATCCCTTGGGCTACTCATGACCACCACTACATCAAACTGACATTTAGACACATAC 814
857 TGGCTCAATGATCCAAAGTTTCAATAGTGGCCACCTCATCTCAGAGAGTGAACATCTCGTAA 916
815 TGGCTCAATGAGCAAAATTTATTGGAACCTTTCTTATACACAGACACCTCAATCCAGAT 874
917 GATCACAAGTATATCTTTTCTCCGTGAAAAATGCAATAGATGAGAGAACTCTGGAATA 976
875 GATGATAAAATATATTTCTTTCTGGAATCATCTCARGAAGGACAGTACTCTCGGATA 934
977 GCTACTCACGCTAGATAGGTTCAGATATGCAAGATGACTTTGAGGGGACAGAAAGTCTG 1036
935 ACCATCTTCTCGAGTTGGAAGATTTTGAAGATGATGTAGAGAGCAACAGCAGCTG 994
1037 GTGAATAATGGACAACATTCCTCAAGCTCGTCTGATTTGCTCAGTGGCAGGTCCAAT 1096
995 ATAAACAAGTGGAGCACTTTTCTTAAGGCCAGACTGATTTGCTCAATTCCTGGAAGT 1054
1097 GGCATTGACACTCATTTTGTATGAATCGCAGGATGATTCCTTAATGAACTTTTAAAGATCCT 1156
1055 GGGCAGATATCTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCCAAGAGATGAA 1114
1157 AAAAAATCCAGTTGATATGAGGTGTTTACGACTTCGATTAACATTTTCAAGGATCAGCC 1216
1115 AGAAATCCTGTAGTATAGGAGTCTTTACTTACAACAGCTCCATCTTCAAGGCTCTGCT 1174
1217 GTGTGATGATAGCATGATGATGAGAGGAGTGTCTTGTGCTCATATGCCACAGG 1276
1175 GTTTGTGTATAGCATGGCTGATCAGAGCAGTTTTAAATGGTCAATATGCTCATAG 1234
1277 GATGGACCCAACTATCAATGGTGGCTTTATCAAGGAAGAGTCCCTTATCACCGCCAGGA 1336
1235 GAAAGTCGACACCATCTGTTGGTGAGTATGATGGGAGATTCCTTATCACCGCTGGT 1294
1337 ACTTGTCCAGCAAAACATTTG---GTGTTTTGACTCTACAAAGAGACCTTCTCTGATGAT 1393
1295 ACATGTCCAAAGCAAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTTCCAGATGAT 1354
1394 GTTATAACCTTTGCAAGAGTCAATCCAGCATCTACATCCAGTGTTCCTATGAACAAT 1453
1355 GTCATCAGTTTCATAAAGCGGCACTCTGTGATGATATAGTCCGTATACCCAGTGGAGGA 1414
1454 CGCCCAATAGTATCAAAACGGAGTAAATATCAATTTACAAATTTGCTGAGACCGA 1513
1415 GGAACCAACGTTCAAGAGAAATCAATGTGGATTACAGACTGACACAGATAGTGGTGGATCAT 1474
1514 GTGGATGCAAGATGACAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1573
1475 GTCATTCGAGAGATGGCCAGTACGATGATGATGATGATGATGATGATGATGATGATGAT 1534
1574 CTTTAAAGTATGTTTCAATTTCTTAAAGAGACTTGGTATGATGATGATGATGATGATGATGAT 1633
1535 CTCAAAGTTGTGACGATTTTCAAGGAAAAGTGG---AATATGGAAGAGGTAGTGTCTGGAG 1591
1634 GAAATCAGAGTGTTCGGGAAACGACTGCTATTTAGCAATGAGAGTTCCTCACTAAGCAG 1693
1592 GAGTTCAGATATTCAGCACTCATCAATCATCTTGAACATGGAATTTCTCTGGAAGCAG 1651
1694 CAACAACTATATATTTGTTTCAACGGCTGGGTTTGGCCAGCTCCCTTTTACACCGGTGTGAT 1753
1652 CAACATTTGATGTTTCCGAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1711
1754 ATTTACGGAAAGCTGTGCTGAGTGTTCCTCGCCGAGACCTTTTACTGTGCTTGGGAT 1813
1712 ACTTATGGGAAAGCTTGCAGACTGTTCTTCTTGGCAGAGACCCCTTACTGTGCTGGAT 1771
1814 GGTTCGCAATGTTCTCGCTATTTTCCACTGCAAGAGAGCAGCAGAGACAGATATA 1873

Db 1772 GGAATGCTCTCGATATGCTCTCTACTTCTAAAGAGAGAGCTAGACGCCAAGATGA 1831
Qy 1874 AGAATGGAGACCCACTGCTACTGTTGAGACTTACACCATGATGATCAATCCATGGCCAC 1933
Db 1832 AAATATGCGACCCCAATCACCAGTCTGGGACATCGAAGACAGCATAGTATCATG--AA 1888
Qy 1934 AGCCCTGAAGAGAGATCATCTATGTTGATAGAGATAGTAGACATTTTGGAAATGCAAT 1993
Db 1889 ACTGCTGATGAAAGGTGATTTTGGCATTTGAATTAATCACTCACTTCTTGGAAATGATA 1948
Qy 1994 CCGAAGTCGAGAGAGCGTGTCTATTTGGCAATTCAGAGCGGAAATGAAGAGCGAAAA 2053
Db 1949 CCTAAATCCCAACAGCAACTATTAAATGGTATATCCAGAGGTGAGGGATGAGCATGA 2008
Qy 2054 GAAGAGATCAGTGGATGATCATATCATCAGACAGATCAAGGCTTCTGCTACGTAGT 2113
Db 2009 GAGGATTTGAGCCGATGAAGATCAATCAAAACGATATGGGCTACTGATTCGAAT 2068
Qy 2114 CTAAACAGAGAGATTAGCAATTAACCTCTGCCATGGGGTGAACATGGGTTTCATACAA 2173
Db 2069 TTGCAAGAGAGATTTCTGGATGTTATCTGCAAGGCCAGGACACATTTTCATCCAC 2128
Qy 2174 ACTCTTCTTAAGGTAAACCTTGAAGTCATTGACACAGAGCATTTTGGAAAGACTTCTTCAT 2233
Db 2129 ACATAGTGAAGTGTACTTGTATGTCATTTGATGATGATGATGATGATGATGATGATGAT 2188
Qy 2234 AAAGATGATGATG 2246
Db 2189 GCAGAGCATGAGG 2201

RESULT 11

US-10-201-858-347
; Sequence 347, Application US/10201858
; Publication No. US20040038337A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCES: E3430R1C464
; CURRENT APPLICATION NUMBER: US/10/201,858
; PRIOR FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION data removed - See File Wrapper or PALM.

; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 347
; LENGTH: 3871
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-201-858-347
Query Match 26.5%; Score 718.6; DB 13; Length 3871;
Best Local Similarity 61.9%; Pred. No. 7.4e-206; Indels 21; Gaps 5;
Matches 1233; Conservative 0; Mismatches 739;
Qy 269 AATGGGAAGAAACAATGTCCTCAAGGCTGAAATATCTTACAAAGAAATGTTGGAAATCCAAC 328
Db 215 ACTTTTGAAGCAAAATATTCTCAAGACTCAAGCTAACTTCAAGAGACTTGTCTGCTTTCAAAT 274
Qy 329 AATGTGATCATTCTCAATGGCTTGGCCAAACAGCTCCAGTTTATCATACCTTCTTTTGGAT 388
Db 275 AGCTGATTTCTCTTTTGGGTTTCATCAGAGGACTGGATTTTCAACTCTTCTCTTAGAT 334
Qy 389 GAGGAACGAGTAGGCTGTATGTTGGAGCAAGAGATCACATATTTTCATTCGACCTGGTT 448
Db 335 GAGGAAGAGAGGAGGCTGCTCTTGGAGCCAAAGACCAACATCTTCTACTCAGTCTGGTT 394
Qy 449 AA---TATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACACCAAGAGAGATGA 505
Db 395 GACITTAACCAAAATTTTAAAGAGATTTTATGGCTCTCTGCAAGAGAACGGTGGAAATTA 454
Qy 506 TCGAAGTGGCTGGAAAGACATCTCTGAAAGAAATGCTTAATTTTCAATCAAGGTACTTAAG 565
Db 455 TGTAAATTTAGCTGGGAAGATGCCAATACAGAAATGTCAAAATTTTCATCAGAGTACTTCAG 514
Qy 566 GCATATATTCAGCTCACTTGTAGCCCTGTGGACGGGGCTTTTTCATCCAAATTTGCACC 625
Db 515 CCTATAACAAACTCACATATATGTTGGAACTGGAGCATTTTATCCAAATATGTGG 574
Qy 626 TACATTGAAATTTGACATCATCTCTGAGGACAAATATTTTAAAGCTGGAGAACTCACATTT 685
Db 575 TATATTGATCTTGGAGTCTACAGAGGAGTATTTATTTCAAACTAGACACACATAATTTG 634
Qy 686 GAAACGGCCGTGGGAGAGTCCATATGACCTTAAGCTGTGACAGCATCCCTTTTAAATA 745
Db 635 GAGTCTGGCAGACTGAAATGCTCTTCATCTCCAGCGCTTTTGTCTTCAATATGACA 694
Qy 746 GATGAGAAATATATCTCTGGAATCTGAGCTGATTTTATGGGCGAGACTTTGCTATCTTC 805
Db 695 GATGAGTACTCTACTCTGGAACAGCTTCTGATTTCTCTGGCAAGATATCTGCAATCACT 754
Qy 806 CGAATCTTTGGGCT 856
Db 755 CGATCCCTTGGGCT 814
Qy 857 TGGCTCAATGATCCAAAGTTCATTTAGTGGCCCACTCATCTCTCAGAGAGTCAATTCCTGAA 916
Db 815 TGGCTCAATGAGCAAAATTTTATTTGAACTTTCTTATACACAGACACCTACATCCAGAT 874
Qy 917 GATGACAAAGTATATCTTTCT 976
Db 875 GATGATAAAATATATTTCT 934
Qy 977 GCTACTCTACGTAGAAATGATGCAAGAAATGATTTTGGAGGCGACAGAAATCTG 1036
Db 935 ACCATCT 994
Qy 1037 GTGATAAATGCAACAATCT 1096
Db 995 ATAAACAAGTGGAGCATTTTCTTTAAGCCAGACTGATTTTCTCAATTTCTTGAAGTGT 1054
Qy 1097 GGCATTTGACATCTTTTGTATGAACTCCAGAGTGTATTTCTTAAATGAACTTTTAAAGATCT 1156
Db 1055 GGGCAGATATCTTACTTTTGTATGAGCTTTCAAGATATTTATTTACTTCCCAACAAGATGAA 1114
Qy 1157 AAAATCCAGTTGTATGAGTGTCTTAACTTCCAGTAAACATTTTCAAGGATCAGGC 1216

Db 1115 AGAAATCCCTGTAGTATATGAGGCTTTTACTACAACCCAGCTCCATCTTCAAGGCTCTGCT 1174
QY 1217 GTGTGTATGTATAGCATGATGATGAGAGGGTGTCCCTTGTCCATATGCCACAGG 1276
Db 1175 GTTGTGTATAGCATGCTGATCAGATCAGAGAGTGTAAATGGTCCATATCTCATAG 1234
QY 1277 GATGGACCCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTTATCCACGGCCAGGA 1336
Db 1235 GAAAGTGCAGACCATCGTTGGGTGAGTATGATGGAGAATTCCTTATCCACGGCTGCT 1294
QY 1337 ACTGTGCCAGCAAAACATTTG---GTGGTGTGACTCTAAGAGACCTTCTCTGATAT 1393
Db 1295 ACATGTCCAAAGCAAAACCTATACCCACTGATTAAGTCCACCCGAGATTTTCCAGATAT 1354
QY 1394 GTTATAACCTTTGCAAGAAAGTCAATCCAGCCATGTACAATCCAGTGTTCCTATGAACAAT 1453
Db 1355 GTATCAGTTTCATAAAGCGGCACCTGTGTATGATATAGTCCGTATACCCAGTTCAGGA 1414
QY 1454 CCCCATAAGTATCAAAACCGGATGTAATTTACAAATTTACAAATTTGTCTAGACCGGA 1513
Db 1415 GGACCAACCTTCAAGAGAAATCAATGTGGATTACAGACTGACACAGATAGTGTGATCAT 1474
QY 1514 GTGGATGACAGAGATGACAGTATGATGTTATGTTTATCGGAACAGATGTTGGACCGTT 1573
Db 1475 GTCATTTGCAAGATGCGCAGTACGATGTAATGTTTCTTGGAAACAGATTTGGAACCTGTC 1534
QY 1574 CTTAAAGTATTTCAATCTTAAGGAGACTTGGTATGATTTTAAAGAGAGTTCGCTGGAA 1633
Db 1535 CTCAAAGTGTGAGCATTTCAAAGGAAAAGTGG---AATATGGAAGAGTAGTGTGAG 1591
QY 1634 GAAATGACAGTTCGGAACCGACTGTATTTTTCAGCAATGAGCTTTCACCTAAGCAG 1693
Db 1592 GAGTTCAGATATTTCAAGCACTCATCAATCATCTTGAACATGGAATTTGCTCTGAAGCAG 1651
QY 1694 CAACAATATATATTTGGTTTCAACGGCTGGGGTGGCCAGCTCCCTTTACACCGGTGTAT 1753
Db 1652 CAACAATGTATATTTGTTCCGAGATGATAGTTTTCAGCTTCCTTGCACAGATGCAC 1711
QY 1754 ATTTACGGAAGAGCTGTGCTGAGTGTGCTTCGCGCCGAGACCTTACTGTCTTGGAT 1813
Db 1712 ACTTATGGGAAAGCTTGGCAGACTGTTGCTTGGCCAGAGACCTTACTGTGCTGGAT 1771
QY 1814 GCTTCTGATGTTCTGCTGATTTTCCACTGCAAGAGACGCAAGAGCAGCAAGATATA 1873
Db 1772 GGAATGATGCTCTGATATGCTCTTCTTCTTAAAGAGAGCTTAGACGCGCAAGATGA 1831
QY 1874 AGAATGAGAGACCCACTGACTCTGTTTACACTTTACACCATGATAATCACCATGGCCAC 1933
Db 1832 AAATATGGCGACCCCAATCACCCAGTGTGGGACATCGAAGACAGCATTAGTCAATG---AA 1888
QY 1934 AGCCCTGAGAGAGATCATCTATGTTGATAGATAGTAGCAGACATTTTGGATGAGT 1993
Db 1889 ACTGCTGATGAAAGAGTATTTTGGCAATGAAATTAACCTCAACCTTCTGGAATGTATA 1948
QY 1994 CCGAAGTGCAGAGAGCGTGTCTTATTTGGCAATTTCCAGAGCGGAAATGAAGAGCGMAAA 2053
Db 1949 CTTAAATCCCAACAGCAACTATTAATAGTATATCCAGAGGTGAGGGGATGAGCATCGA 2008
QY 2054 GAAGATCAGAGTGTATGATCATATCATCAGGACAGATCAAGGCTTCTGCTAGTGTAGT 2113
Db 2009 GAGGAGTTGAAGCCCGATGAAGAGATCATCAAAACGGAATATGGCTACTGATTCGAAGT 2068
QY 2114 CTACAACAGAGATTCAGGCAATTTACCTCTGCCATGCGGTGGAAACATGGGTTCATACAA 2173
Db 2069 TTGAGAGAGAGATTTCTGGATGTATTACTGCAAGCCGAGGACACACTTTTATCCAC 2128
QY 2174 ACTCTTTTAAAGTAAACCTGGAAGTCAATGACACAGAGCATTTGGAAGAACTTTCTTAT 2233
Db 2129 ACCATAGTGAAGCTGACTTTGAATGTCTATGAGATGAACAGATGGAATAATACCAGAGG 2188
QY 2234 AAAGATGATGATG 2246
Db 2189 GCAGAGCATGAGG 2201

RESULT 12

US-10-205-890-347
; Sequence 347, Application US/10205890
; Publication No. US20040048334A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C519
; CURRENT APPLICATION NUMBER: US/10/205,890
; PRIOR FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 347
; LENGTH: 3871
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-205-890-347

Query Match 26.5%; Score 718.6; DB 13; Length 3871;
Best Local Similarity 61.9%; Pred. No. 7.4e-206;
Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;
QY 269 AATGGGAGAACATGTGCCAGGCTGAAATTCCTCAAGAAATGTTGGATCCAC 328
Db 215 ACTTGAAGCAAAATATTCAGACTCAAGCTAACCTCAAGAGACTTGTCTTCAAT 274
QY 329 AATGTGATCACTTTCAATGGCTTGGCCAGCTCCAGTTATCATACCTTCTTTTGGAT 388
Db 275 AGCTGATATCCCTTTTGGTTTCATCAGAGGACTGGATTTTCAAACTCTTCTTAGAT 334
QY 389 GAGGAACGAGTAGGCTGTATGTGGAGCAAGGATCACAATTTTCNTTCGACCTGGTT 448
Db 335 GAGGAAGAGGAGGCTGTCTTGGAGCCAAAGACCATCTTCTACTCATGCTCTGGTT 394
QY 449 AA---TATCAAGATTTTCAAAAGATTGTGTGCCAGTATCTTACACCAAGAGAGATGAA 505
Db 395 GACTTAAACAAAATTTTAAAGAGATTATTGGCTCTGCTCAAGAGAAACGGGTGGATTA 454
QY 506 TCGAAGTGGCTGGAAAAGACATCTCGAAGAAATGTGCTAAATTCATCAAGGTACTTAAG 565

Db 455 TGTAATAGCTGGGAAAGATGCCAATACAGAAATGTGCAAAATTCATCAGAGTACTTCAG 514
Qy 566 GCATATAATCAGACTCAGCTGTGAGCTGTGAAAGGGGGCTTTTCATCCAAATTTGCAAC 625
Db 515 CCCTATAACAAACTCAGATATATGTGTGGAATCTGGAGCATTTATCCCATATGTGGG 574
Qy 626 TACATTGAATTTGGAGCATCATCTGAGGACAATATTTTTTAAGCTGGAGAACTCAGATTTT 685
Db 575 TATATTGATCTTGGAGCTTCAAGGAGGATATATATTTCAAACTAGACACATAAATTTG 634
Qy 686 GAAAGCGGCGTGGGAAAGTCCATATGACCCCTAAGCTGTGACAGCATCCCTTTTAATA 745
Db 635 GAGTCTGGCAGACTGAATGTCTTCGATCTCAGCAGCTTTTGTCTCAGTAATGACA 694
Qy 746 GATGGAGATTAATCTCTGGAATCTGAGCTGATTTTATGGGCGGAGACTTTGCTATCTTC 805
Db 695 GATGAGTACTCTACTCTGGAAGAGCTTCTGATTTCTTGGCAAGATACTGCAATTCAT 754
Qy 806 CGAATCTTGGGC-----ACCACCCCAATCAGGACAGCAGCATGATTTCCAGG 856
Db 755 CGATCCCTTGGGCTACTCATGACCACTACATCAGACTGACATTTGAGCAGCATAC 814
Qy 857 TGCTGATGATCCAAAGTTCAATAGTGGCCCACTCATCTCAGAGAGTGAATCTCTGAA 916
Db 815 TGCTGATGATCCAAAGTTCAATAGTGGCCCACTCATCTCAGAGAGTGAATCTCTGAA 874
Qy 917 GATGACAAAGTATATCTTCTTCTGGAATGCAATGATGAGGAGACATCTCTGAA 976
Db 875 GATGATTAATATATTTCTTCTGGAATGCAATGATGAGGAGACATCTCTGAA 934
Qy 977 GCTACTCAGCTAGAAATAGTCAATATGCAAGATGATGAGGAGACATCTCTGAA 1036
Db 935 ACCATCTTCTGAGTGGGAGAGTTTGAAGATGATGAGGAGACATCTCTGAA 994
Qy 1037 GTCAATAATGGGACAACTTCTCAAGCTCTGCTGATTTGCTCAGTCCAGGTCCTCAAT 1096
Db 995 ATAAACAGTGGAGAGCTTTCTTAAGCCAGACTGATTTGCTCAATCTCTGGAAGTAT 1054
Qy 1097 GGCATGACACTCAATTTGATGAACTGAGGATGATTTCTTAAGTAACTTTAAAGATCT 1156
Db 1055 GGGGCGAGATCTTACTTGTAGCTTCAAGATATTTATTTACTCCCAAGAGATGAA 1114
Qy 1157 AAAAAATCCAGTTGATATGAGTGTATACAGCTTCCAGTAACTTTTCAAGGAGTACGCC 1216
Db 1115 AGAATCTCTGATATGAGTCTTTACTACAACTGATTTCAAGGCTTCAAGGCTTCTGCT 1174
Qy 1217 GTGTGATGATAGCTAGTATGAGAGGGTGTCTTGTGTCATATGCCCCAAGG 1276
Db 1175 GTTTGTGTATAGCATGCTGACATCAGAGCAGTTTTTAATGCTCCATATGCTCATAG 1234
Qy 1277 GATGGACCAACTATCAATGGTGTCTTATCAAGGAGAGTCCCTATCCAGGCCAGGA 1336
Db 1235 GAAAGTGCAGACATCTGTTGGTGCAGTATGATGGAGAAATCTTATCCAGGCTTGT 1294
Qy 1337 ACTGTGCCAGCAAAACATTTG---GTGTTTTGATCTTCAAGGAGCTTTCTGATGAT 1393
Db 1295 ACATGTCCAAGCAAAACCTATGACCACTGATTAAGTCCACCGAGATTTTCCAGATGAT 1354
Qy 1394 GTTATAACCTTTGCAAGAGTATCATCCAGCATGATCAATCCAGTGTCTTCTATGAAAT 1453
Db 1355 GTCATCAGTTTCAAGAGGAGCTCTGTGATGATGATGATGATGATGATGATGATGAT 1414
Qy 1454 CGCCCAATAGTATCAAAACCGAGTAAATTAATTAATTAATTAATTAATTAATTAATTAAT 1513
Db 1415 GGACCAAGCTTCAAGAGATCAATGTGGATTAAGTATGATGATGATGATGATGATGATGAT 1474
Qy 1514 GTGGATGCAAGAGATGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1573
Db 1475 GTCAATTTGCAAGAGATGCAAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1534
Qy 1574 CTTAAAGTATGATTTCAATTTCAAGGAGTATGATGATGATGATGATGATGATGATGATGAT 1633
Db 1535 CTTAAAGTATGATTTCAAGGAGTATGATGATGATGATGATGATGATGATGATGATGATGAT 1591

Qy 1634 GAAATGACAGTTTTTCGGGAAACCGAGTGTCTATTTTTCAGCAATGGAGCTTTCCACTAAGCAG 1693
Db 1592 GAGTTGAGATATTTCAAGCACTCATCAATCATCTTTGAACATGGAATTTCTCTGAAGCAG 1651
Qy 1694 GAACTACTATATATTTGGTTCAACGGTGGGGTTCGCCAGCTCCCTTTTACACCGGTGTGAT 1753
Db 1652 CAACAAATTTGATTTGGTTCCCGAGATGATTTAGTTCAGCTCTCTTTTGCACAGTGGAC 1711
Qy 1754 ATTTACGGGAAAGCGTGTGCTGAGTGTTCCTCCCGGAGACCTTTACTGTCTGCTGGAT 1813
Db 1712 ACTTATGGGAAAGCTTGGCAGACTGTTGCTTCCAGAGACCTTACTGTGCTGGAT 1771
Qy 1814 GGTCTGATGTTCTGCTATTTTCCCACTGCAAGAGAGAGCAGACAGAGATATA 1873
Db 1772 GAAATGATGCTCTGATATGCTCTTCTTCTTAAAGGAGAGTACAGCCCAAGATGTA 1831
Qy 1874 AGAAATGAGAGCCCACTGACTCACTGTTCAGACTTACACCATGATATATCAACCATGGCCAC 1933
Db 1832 AATATGCGACCCCAATCACCCAGTGTGGACATCGAAGACAGCATTTAGTCTATG---AA 1888
Qy 1934 AGCCCTGAGAGAGATCATCTATGTTGTAGAGATAGTAGCAGATTTTGGATGAGT 1993
Db 1889 ACTGTGATGAAAGGAGTATTTTGGCATTTGAATTAACCTCAACCTTTCTGGAATGATATA 1948
Qy 1994 CCGAAGTCCGAGAGAGCGCTGCTCTATTGGCAATTTCCAGAGGCGAAATGAAGAGCGAAAA 2053
Db 1949 CCTAATCCCAAGCAACTATTAAATGTTATATCCAGAGTTCAGGGATGAGCATCGA 2008
Qy 2054 GAAGATCAGAGTGGATGATCATCATCAGGACAGATCAGGCTTTCTGCTAGCTAGT 2113
Db 2009 GAGGAGTTGAAAGCCCGATGAAAGAAATCATCAAAACCGAATATGGGCTTACTGATTCGAAGT 2068
Qy 2114 CTACACAGAGAGGATTCAGGCAATTTACTCTGCTCATCGGTGGAAACATGGTTCTATACAA 2173
Db 2069 TTGCAGAGAGAGGATTTCTGGATGATTTACTTGCAAAACCCAGGAGCAGACTTTTCTATCCAC 2128
Qy 2174 ACTCTTTTAAAGTAAACCTGGAAGTATTTGACAGAGATTTGAGAGACTTTCTTCAT 2233
Db 2129 ACCATAGTGAAGCTGACTTTGAATGTCATTTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 2188
Qy 2234 AAGATGATGATG 2246
Db 2189 GCAGAGCATGAGG 2201

RESULT 13

US-10-208-024-347
; Sequence 347, Application US/10208024
; Publication No. US20040048335A1

GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Goddard, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430R1C538

; CURRENT APPLICATION NUMBER: US/10208,024

; PRIOR FILING DATE: 2002-07-29

; PRIOR APPLICATION NUMBER: 10/052586

; PRIOR FILING DATE: 2002-01-15

; PRIOR APPLICATION NUMBER: 60/059263

; PRIOR FILING DATE: 1997-09-18

; PRIOR APPLICATION NUMBER: 60/059266

; PRIOR FILING DATE: 1997-09-18

;; PRIOR APPLICATION NUMBER: 60/062250
;; PRIOR FILING DATE: 1997-10-17
;; PRIOR APPLICATION NUMBER: 60/063120
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063121
;; PRIOR FILING DATE: 1997-10-24
;; PRIOR APPLICATION NUMBER: 60/063486
;; PRIOR FILING DATE: 1997-10-21
;; PRIOR APPLICATION NUMBER: 60/063540
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063541
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION NUMBER: 60/063544
;; PRIOR FILING DATE: 1997-10-28
;; PRIOR APPLICATION data removed - See File Wrapper or PALM.
;; NUMBER OF SEQ ID NOS: 612
;; SEQ ID NO 347
;; LENGTH: 3871
;; TYPE: DNA
;; ORGANISM: Homo Sapien
US-10-208-024-347

Query Match 26.5%; Score 718.6; DB 13; Length 3871;
Best Local Similarity 61.9%; Pred. No. 7.4e-206;
Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;

QY	269	AATGGGAACAACATCTGCCAAGGCTGAAATTCCTACAAAGAAATGTTGAAATCCAAAC	328
DB	215	ACTTTGAACAAAATATCCAAAGCTCAAGCTAACTCAAAAGACTTCTGCTCTTCAAAT	274
QY	329	AATGTGATCATTTCATATGGCTTGGCCAAACAGCTCCAGTTATCATACCTTCCTTTGGAT	388
DB	275	AGCTGATTCCTTTTGGGTTTCATCAGAAGGACTGGATTTTCAAACCTCTCTCTTAGAT	334
QY	389	GAGGAACGAGTAGGCTGTATGTTGGAGCAAGGATCACAATTTTTCATTCGACCTGGTT	448
DB	335	GAGGAAGAGGAGGCTGCTCTTGGAGCCAAAGACCAATCTTTCTACTCAGTCTGGTT	394
QY	449	AA---TATCAAGATTTTCAAAGATTTGTGGCCAGTATCTTACACCAAGAGATGAA	505
DB	395	GACTTAAACAAAATTTTAAAGAGATTTATTTGGCTCTGCAAGGACGGGTGGAATTA	454
QY	506	TGCAAGTGGCTGGAAAGACATCTCTGAAAGAAATGTGTAATTTTCAACAGGTAATTAA	565
DB	455	TGTAAATAGCTGGGAAGATGCCAATACAGAATGTGCAAAATTTTCATCAGAGTACTTCAG	514
QY	566	GCATATAACAGACTCACTTTACGCTGTGGAACGGGGCTTTTCATCCAAATTTGCACC	625
DB	515	CCCTATAACAAACCTCACATATATGTGTGGAATCTGGAGCAATTTTCATCCAAATAGTGG	574
QY	626	TACATTGAAATGGACATCATCTCGAGGCAATATTTTAACTGGAGAACTCAATTTT	685
DB	575	TATATTGATCTTGGAGCTTACAAGGAGGATATTATATCAAACCTAGACACACATAATTTG	634
QY	686	GAAACGGCGTGGGAGAGTCCATATGACCTAGCTGCTGACAGCATCCCTTTTAATA	745
DB	635	GAGTCTGGCAGACTGAAATGTCTTTCGATCTCTCAGCAGCCTTTTTCGTTTCAAGTAATGAC	694
QY	746	GATGAGAAATTAATCTCTGGAATCGAGCTGATTTTATGGGCGAGACTTTTCTGATCTTC	805
DB	695	GATGAGTACCTTACTCTGGAACAGCTTCTGATTTCTTCCCTGGCAAGATGACTGCATTCAT	754
QY	806	CGAATCTTTGGG-----ACACACCCCAATCAGGACAGAGCAGCATGATTCAGG	856
DB	755	CGATCCCTTTGGGCTACTCATGCCACCACTACATCAGAACTGACATTTTCAGAGCACTAC	814
QY	857	TGCTCAATGATCCAAAGTTTCAATAGTGCCCACTCATCTCAGAGAGTGACAACTCCTGAA	916
DB	815	TGGCTCAATGGAGCAAAATTTTATGGAACTTTTCTTACACAGACACCTACAAATCCAGAT	874
QY	917	GATGACAAAGTATACCTTTTCTCCGTGAAATGCAATAGATGGAACACATCTCTGAAAA	976
DB	875	GATGATAAAATATATTTCTTTCTTTCTGTAATCATCTCAAGAGGCGAGTACCTCCGATAAA	934

QY	977	GCTACTCACGCTAGAAATAGGTTCAGATGATGCAAGATGACTTTTGGAGGGGACAGAACTCTG	1036
DB	935	ACCATCCTTTCTCGAGTTGGAAGAGTTTGTAAAGATGATGTAGGAGGACACGACGCTG	994
QY	1037	GTGAATAAATGGACAACATTCCTCAAGCTCGCTGATTTTGTCTCAGTGCCAGGTCCAAAT	1096
DB	995	ATMAACAAGTGGAGGACTTTTCTTAGGCCAGACTGATTTTCTCAATTTCTTGAAGTGTAT	1054
QY	1097	GGCATTGCACACTCATTTTGTAGTGAACACTGCAGATGTATTCCTAATGAACTTTTAAAGATCCT	1156
DB	1055	GGGCGAGATACTTACTTTGATGAGCTTCAAGATATTTATTTACTCCCAACAAGAGATGAA	1114
QY	1157	AAAAATCCAGTTGTATATGAGTGTATACGACTTCAGATAACATTTTCAAGGATCAGCC	1216
DB	1115	AGAAATCCTGTATATGAGGCTTTTACTACAAACAGCTCCATTTTCAAGGCTCTGCT	1174
QY	1217	GTGTGTATGTATAGCATGAGTGTGAGAAGGGTGTCTCTGTCATATGCCACAGG	1276
DB	1175	GTTTGTGTATAGCATGGCTGACATCAGAGCAGTTTATTAATGGTCCATATGCTCATAG	1234
QY	1277	GATGGACCCAACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTTATCCACGGCCAGGA	1336
DB	1235	GAAAGTCAGACCACTCGTTGGGTGCAATGATGGGAGAAATCCTTATCCACGGCCTGGT	1294
QY	1337	ACTTGTCCCAAGCAAAACATTTG---GTGGTTTGTACTCTACAAAGGACCTTCTCTGATGAT	1393
DB	1295	ACATGTCCAAGCAAAACCTATGACCCACTGATTAAGTCCACCCGAGATTTTCCAGATGAT	1354
QY	1394	GTTATAACCTTTTGCAGAAGTGTATCCAGCCATGTACATCCAGTGTTCCTATGAACAAT	1453
DB	1355	GTCAATCAGTTTCTATAAAGCGGCATCTGTGATGTATAAGTCCGTATATACCCAGTTGCAGGA	1414
QY	1454	CGCCCAATAGTATCAAAACGGATGTAATTAACAATTTACAAATTTGCTGTAGACCGA	1513
DB	1415	GGACCAAGCTTCAGAGAATCAATGTGGATTACAGCTGCACAGATAGTGTGGTGCAT	1474
QY	1514	GTGGATCGAGAAGATGGACATGATGATGTTATGTTATCGGAAACAGATTTTGGGACCGTT	1573
DB	1475	GTCAATTCAGAAGATGGCCAGTACGATGTAATGTTCTTGGAAACAGACATTTGGAATGTC	1534
QY	1574	CTTAAAGTAGTTTCAATTCCTTAGGAGACTTGTATGATGATTAGAGAGGTTCTCTGGAA	1633
DB	1535	CTCAAGTTTGTACGATTTCAAAGGAAAAGTGG---AATATGGAAGAGGTTAGTGTGGAG	1591
QY	1634	GAAATGACAGTTTTCGGGAACCGACTGTCTATTTACAGCAATGGAGCTTTTCCACTAAGCAG	1693
DB	1592	GAGTTGCAGATATTCAGACTCATCAATCATCTTGAACATGAAATTTCTCTGAAGCAG	1651
QY	1694	CAACAATATATATTTGTTCAACGGCTGGGGTTGCCAGCTCCCTTTTACACCGGTGTGAT	1753
DB	1652	CAACAATTTGATGTTTCCCGAGATGGAATTAAGTTTCACTCTCTTTCACAGATGCGAC	1711
QY	1754	ATTTACGGGAAAGGCTGTGTGAGTGTGCTCGCCGAGACCTTACTGTCTTGGGAT	1813
DB	1712	ACTTATGGGAAAGCTTCCGAGACTGTGTTCTTGGCAGAGACCCCTACTGTGCTGGAT	1771
QY	1814	GGTTCTGCATGTTCTGCTATTTTCCACTGCAAAAGAGACGCAAGACACAGATATA	1873
DB	1772	GGAAATGCATGCTCTCGATATGCTCTACTTCTTAAAGGAGAGCTAGACGCCAAGATGTA	1831
QY	1874	AGAAATGGAGACCCACTGACTCATGTTTCAGACTTACACCATGATATACCATGGCCAC	1933
DB	1832	AAATATGGGACCCCAATCACCCAGTGTGGGACATCGAAGACAGCATTAGTCTATG---AA	1888
QY	1934	AGCCCTGAAGAGAGAATCATCTATGTTGTAGAAATAGTAGACATTTTGGAAATGCAAT	1993
DB	1889	ACTGCTCATGAAAGGTTGATTTTGGCATTGAAATTTAACTCAACCTTTCTTCTGGAATGATA	1948
QY	1994	CCGAAGTCGAGAGAGCGCTGTCTATTGCAATTCAGAGGGGAAATGAGAGCGGAAAA	2053
DB	1949	CCTAAATCCCAACAGCAACTATTAAATGTTATATCCAGAGGTGACGGGATGAGCATCGA	2008

QY 2054 GAAGAGATCAGATGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTACGTAGT 2113
 DB 2009 GAGGAGTTGAAGCCGATGAAGAATCATCAAAACGGAATATGGGCTACTGATTCGAGT 2068
 QY 2114 CTACACAGAAGGATTCAGGCAATTAACCTCTGCCATCGGCTGGAAACATGGGTTTCATACAA 2173
 DB 2069 TTGACAGAGAGGATTCCTGGATGTATTAATGCAAGCCAGGAGACACATTTTCATCCAC 2128
 QY 2174 ACTCTTTTAAAGGTAAACCTCGGAAGTCTATGACACAGAGCATTTGGAAGAACTTCTTCAT 2233
 DB 2129 ACCATAGTGAAGCTGACTTTGAATGTCTATGAGAATGAACAGATGGAAGAAATACCCAGAGG 2188
 QY 2234 AAAGATGATGATG 2246
 DB 2189 GCAGAGCATGAGG 2201

RESULT 14
 US-10-201-853-347
 ; Sequence 347, Application US/10201853
 ; Publication No. US20040053358A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Baker, Kevin P.
 ; APPLICANT: Chen, Jian
 ; APPLICANT: Desnoyers, Luc
 ; APPLICANT: Goddard, Audrey
 ; APPLICANT: Godowski, Paul J.
 ; APPLICANT: Gurney, Austin L.
 ; APPLICANT: Pan, James
 ; APPLICANT: Smith, Victoria
 ; APPLICANT: Watanabe, Colin K.
 ; APPLICANT: Wood, William I.
 ; APPLICANT: Zhang, Zemin
 ; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
 ; TITLE OF INVENTION: ACIDS ENCODING THE SAME
 ; FILE REFERENCE: P3430R1C465
 ; CURRENT APPLICATION NUMBER: US/10/201,853
 ; PRIORITY FILING DATE: 2002-07-23
 ; PRIOR APPLICATION NUMBER: 10/052586
 ; PRIOR FILING DATE: 2002-01-15
 ; PRIOR APPLICATION NUMBER: 60/059263
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/059266
 ; PRIOR FILING DATE: 1997-09-18
 ; PRIOR APPLICATION NUMBER: 60/062250
 ; PRIOR FILING DATE: 1997-10-17
 ; PRIOR APPLICATION NUMBER: 60/063120
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063121
 ; PRIOR FILING DATE: 1997-10-24
 ; PRIOR APPLICATION NUMBER: 60/063486
 ; PRIOR FILING DATE: 1997-10-21
 ; PRIOR APPLICATION NUMBER: 60/063540
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063541
 ; PRIOR FILING DATE: 1997-10-28
 ; PRIOR APPLICATION NUMBER: 60/063544
 ; PRIOR FILING DATE: 1997-10-28
 ; Prior Application data removed - See File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 612
 ; SEQ ID NO 347
 ; LENGTH: 3871
 ; TYPE: DNA
 ; ORGANISM: Homo Sapien
 ; US-10-201-853-347

Query Match 26.5%; Score 718.6; DB 13; Length 3871;
 Best Local Similarity 61.9%; Pred. No. 7.4e-206;
 Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;

QY 269 AATGGGAAGCAATGTCCAGGCTGAATATCTACNAAGAAATCTTGAATCCCAAC 328
 DB 215 ACTTGAAGCAAAATATTCAGAGACTCAAGCTAACTACAAAGACTTCTGCTTCAAT 274

QY 329 AATGTGATCACATTTCAATGGCTTGGCCAAACAGCTCCAGTTATCATACCTTCTCTTTGGAT 388
 DB 275 AGCTGTATTCCTTTTGGGTTTCATCAGAAGACTGGATTTTCAAACTTCTCTCTTAGAT 334
 QY 389 GAGGAACGAGTGTATGTGTGGAGCAAGGATCAATATTTTCAATTCGACTGGTT 448
 DB 335 GAGGAAGAGGCGAGCTGTCTTGGGAGCCAAAGACCACTCTTTTACTCAGTCTGGTT 394
 QY 449 AA---TATCAAGGATTTTCAAAAGATTCTGTGGCCAGTATCTTACACCAGAAGAGATGAA 505
 DB 395 GACTTAACAAATAATTTAAGAGATTTTATGGCTGTCTCAAGGACGGGTGAATTA 454
 QY 506 TGCAAGTGGCTGGAAAGACATCTCTGAAAGATGTGCTAATTTTCAATCAAGTACTTAAG 565
 DB 455 TGTAAATTAGCTGGGAAAGATGCCAATACAGAAATGTCAAAATTTTCATCAGAGTACTTCAG 514
 QY 566 GCATATATCAGACTCACTTGTACGCTGTGGAACGGGGCTTTTTCATCCAAATTTGCACC 625
 DB 515 CCTATAACAAACCTACATATATGTGTGGAACCTGGAGCATTTTCATCCATATGTGGG 574
 QY 626 TACATTTGAAATTTGGACATCATCTCTGAGGACATATTTTAAAGCTGGAGAACTCAATTTT 685
 DB 575 TATATTGATCTTGGAGTCTTCAAGGAGGATATTAATTCAAACTAGACACACATAAATTG 634
 QY 686 GAAAACGGCGTGGGAAGTCCATATGACCTAGCTGTCTGACAGCATCCCTTTTAATA 745
 DB 635 GAGTCTGGCAGACTGAAATTTGCTTTTCGATCTCAGCAGCTTTTGTCTTCAGTAATGACA 694
 QY 746 GATGGAGATTAATTAATCTTGGAACTGAGCTGATTTTATGGGCGGAGACTTTGCTATCTTC 805
 DB 695 GATGAGTACTCTACTCTTGGACAGCTTCTGATTTCCCTGGCAAGATAGTCAATCACT 754
 QY 806 CGAATCTTTGGGC-----ACCACACCCAAATCAGACACAGCAGCATGATTCAGG 856
 DB 755 CGATCCCTTTGGGCTTACTCATGACCACCACACTACATCAGAACTGACATTTTCAGAGCACTAC 814
 QY 857 TGGCTCAATGATCCAAAGTTCATTAGTGCCCACTCATCTCAGAGAGTGACAAATCCTGAA 916
 DB 815 TGSCTCAATGGAGCAAAATTTAATGGAATTTTCTTACACAGACACCTACATCCAGAT 874
 QY 917 GATGACAAAGTATATCTTTTCTTCCGTGAAATGCAATAGATGGAGAACATCTCGAATAA 976
 DB 875 GATGATAAAATATATTTCTTCTTTCGTGAATCATCTCAAGAGGCGAGTACCTCCGATAA 934
 QY 977 GCTACTCAGCTAGATAGTGCAGATATGCAAGATGATTTTGGAGGGCAGACAGAGTCTG 1036
 DB 935 ACCATCCTTTCTCGAGTTGGAAAGATTTGTAAGAATGATGTAGGAGGACACGAGCCTG 994
 QY 1037 GTGAATAAATGGACAAACATTCCTCAAGCTCGTCTGATTTGTCTAGTCCAGGTCCAAAT 1096
 DB 995 ATAAACAGAGTGGAGCGACTTTCTTAAGGCCAGACTGATTTGTCTCAATTCCTGGAAGTGA 1054
 QY 1097 GGCATTTGACATCACTTTTCAATGAACTGAGGATGATTTCTTAATGAATTTTAAAGATCCT 1156
 DB 1055 GGGGCGAGATCTTACTTGTGAGCTTCAAGATATTTATTTCTCCCAACAGAGATGAA 1114
 QY 1157 AAAAATCCAGTTGTATATGAGTGTTCAGACTTCCAGTAAACATTTTCAAGGGATCAGCG 1216
 DB 1115 AGAAATCCTGTAGTATATGAGTCTTTACTACACAGCTCCATCTTCAAGGGCTCTGCT 1174
 QY 1217 GTGTGATGTATAGCATAGTGTGAGAGGGGTTCCTTGGTTCATATGCCACAGG 1276
 DB 1175 GTTTGTGTATAGCATGGCTGACATCAGAGCAGTTTAAATGGTCCATATCTCATAG 1234
 QY 1277 GATGGACCCCACTATCAATGGGTGCTTATCAAGGAAGAGTCCCTTATCCAGGGCAGGA 1336
 DB 1235 GAAAGTGCAGACCATCGTTGGGTGAGTATGATGGAGAAATTCCTTATCCACGGCTGCT 1294
 QY 1337 ACTTGTCCAGCAAAACATTTG---GTGTTTGTGCTTACAAAGACCTTCTCTATGAT 1393
 DB 1295 ACATGTCCAAGCAAAACCTATGACCACCTGATTAAGTCCACCCGAGATTTTCCAGATGAT 1354

Qy	1394	GTATATACTTTGCAAGAAGTCATCCAGCCATGTACAATCCAGTGTTCCTATGAACAAT	1455
Db	1355	GTCAATCACTTTCTAAAGCGGCATCTCTGTATGTATAAGTCCGTATACCCAGTTGCAGGA	1414
Qy	1454	CGCCCAATAGTGATCAAAACGGATGTAAATATCAATTTACAAATTTGTCGTAGACCGA	1513
Db	1415	GGACCAACGTTCAAGAGAAATCAATGTGGAATACAGACTGACACAGATAGTGTGGATCAT	1474
Qy	1514	GTGGATCCAGAAGATGGACAGTAGTAGTTATGTTTATCCGACACAGATGTTGGGACCGTT	1573
Db	1475	GTCAATTCAGAAGATGGCCAGTAGTAGTATGTATTTCTTGGAAACAGACATTTGGAACCTGC	1534
Qy	1574	CTTAAAGTAGTTTCAATTTCTTAAGGAGACTTGGTATGATTTAGAAGAGGTTCTCTCTGGAA	1633
Db	1535	CTCAAGTTGTACAGCAATTCAGAGAAAGTGG---NATATGAGNAGAGGTAGTGTCTGGAG	1591
Qy	1634	GAATGACAGTTTTTCGGGAACCGACTGCTATTTACGAAATGGAGCTTTCCACTAAGCAG	1693
Db	1592	GAGTTGCAGATATTTCAAGCACTCATCAATCATCTTGAACATGGAATGTCTCTGAAGCAG	1651
Qy	1694	CAACAACATATATTGTTTCAACGGCTGGGGTTGCCAGCTCCCTTTTACACCGGTGTGAT	1753
Db	1652	CAACAATGTACATTTGTTCCCGAGATGGAATAGTTCAGTCTCTTTGCAAGATGGCAG	1711
Qy	1754	ATTTCACGGGAAAGCGTGTGTGAGTGTGGCTGCGCCGAGACCCCTACTCTGTCTGGGAT	1813
Db	1712	ACTATGGGAAAGCTTCGCGACAGCTGTGTCTTCCAGAGACCCCTACTGTGCTGGAT	1771
Qy	1814	GGTTCTGCATGTTCTCGCTATTTTCCCACTGCAAGAGAGCGCAAGACACAGATATA	1873
Db	1772	GGAAATGCATGCTCTCGATATGCTCTACTTCTTAAAGGAGAGCTAGACGCCAAGATGA	1831
Qy	1874	AGAAATGGAGACCCACTGACTCACTGTTTCAGACTTACACCATGATATACCATGGCCAC	1933
Db	1832	AAATATCGGACCCCAATCAACCACTGTGGGACATCGAAGACGATTAGTCATG---AA	1888
Qy	1934	AGCCCTGAAGAGAGAATCATCTATGTGTAGAGAATAGTAGCAATTTTGGAAATGCAGT	1993
Db	1889	ACTGCTGATGAAAAAGGTGATTTTGGCATGTGAATTTAACTCAACCTTCTCGAATGTATA	1948
Qy	1994	CCGAAGTCGAGAGAGCGCTGGTCTATTGGCAATTCAGAGGCGAATAGAGACGAAAA	2053
Db	1949	CCTAAATCCCAACAAGCAACTATTAATATGGTATATCCAGAGGTGAGGGATAGCATCGA	2008
Qy	2054	GAAGAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCCCTTCTGCTACGTAGT	2113
Db	2009	GAGGAGTTGAAGCCCGATGAAGAATCATCAAAACGGAATATGGCTACTGATTCGAAGT	2068
Qy	2114	CTACAACAGAAGAGATTCAGGCAATTACTCTGCCATCCGTTGGNACATGGTTCATACAA	2173
Db	2069	TTGCAGAAGAGGATTCCTGGGATGTATTCTGCAAAAGCCCGAGGAGCACTTTTCATCCAC	2128
Qy	2174	ACTCTTCTTAAGGTAAACCTCGGAAGTCATTGACACAGAGCATTTGGAAAGAACCTCTTCAT	2233
Db	2129	ACCATAGTAGCTGACTTTGAAATGTCAATGAGAAATGACAGATGGAANAATACCCAGAGG	2188
Qy	2234	AAAGATGATGATG	2246
Db	2189	GCAGCATGAGG	2201

RESULT 15
US-10-174-581-347
; Sequence 347, Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Lian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James

; PRIOR APPLICATION NUMBER: 60/080333
 ; PRIOR FILING DATE: 1998-04-01
 ; PRIOR APPLICATION NUMBER: 60/081049
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081070
 ; PRIOR FILING DATE: 1998-04-08
 ; PRIOR APPLICATION NUMBER: 60/081195
 ; PRIOR FILING DATE: 1998-04-09
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 ; PRIOR APPLICATION NUMBER: 60/083559
 ; PRIOR FILING DATE: 1998-04-29
 ; PRIOR APPLICATION NUMBER: 60/084366
 ; PRIOR FILING DATE: 1998-05-05
 ; PRIOR APPLICATION NUMBER: 60/084414
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 ; PRIOR FILING DATE: 1998-05-15
 ; PRIOR APPLICATION NUMBER: 60/086023
 ; PRIOR FILING DATE: 1998-05-18
 ; PRIOR APPLICATION NUMBER: 60/086392
 ; PRIOR FILING DATE: 1998-05-22
 ; PRIOR APPLICATION NUMBER: 60/086486
 ; PRIOR FILING DATE: 1998-05-22
 ; PRIOR APPLICATION NUMBER: 60/087098
 ; PRIOR FILING DATE: 1998-05-28
 ; PRIOR APPLICATION NUMBER: 60/087208
 ; PRIOR FILING DATE: 1998-05-28
 ; PRIOR APPLICATION NUMBER: 60/087609
 ; PRIOR FILING DATE: 1998-06-02
 ; PRIOR APPLICATION NUMBER: 60/087759
 ; PRIOR FILING DATE: 1998-06-02
 ; PRIOR APPLICATION NUMBER: 60/087827
 ; PRIOR FILING DATE: 1998-06-03
 ; PRIOR APPLICATION NUMBER: 60/088025
 ; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/088028
 ; PRIOR FILING DATE: 1998-06-04
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 ; PRIOR FILING DATE: 1998-06-04
 ; PRIOR APPLICATION NUMBER: 60/088033
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 ; PRIOR APPLICATION NUMBER: 60/088167

; PRIOR FILING DATE: 1998-06-05
 ; PRIOR APPLICATION NUMBER: 60/088202
 ; PRIOR FILING DATE: 1998-06-05
 ; PRIOR APPLICATION NUMBER: 60/088212
 ; PRIOR FILING DATE: 1998-06-05
 ; PRIOR APPLICATION NUMBER: 60/088217
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 ; PRIOR APPLICATION NUMBER: 60/089512
 ; PRIOR FILING DATE: 1998-06-16
 ; PRIOR APPLICATION NUMBER: 60/089514
 ; PRIOR FILING DATE: 1998-06-16
 ; PRIOR APPLICATION NUMBER: 60/089538
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089598
 ; PRIOR FILING DATE: 1998-06-17
 ; PRIOR APPLICATION NUMBER: 60/089653

Query Match 26.5%; Score 718.6; DB 13; Length 3871;
 Best Local Similarity 61.9%; Pred. No. 7.4e-206;
 Matches 1233; Conservative 0; Mismatches 739; Indels 21; Gaps 5;

QY 269 AATGGGAAGAACAAATGTGCCAAGGCTGAAATATCTTACAAAGAAATGTTGGAATCCAC 328
 DB 215 ACTTTGAAGCAAAATATTCCTCAAGCTCAAGCTAACCTACAAAGACTTGTCTTCAAT 274
 QY 329 AATGTGATCACTTCAATGCTTGCCCAACAGCTCCAGTTATCATACCTTCCTTTTGAT 388
 DB 275 AGCTGATTCCTCTTTTGGGTTTCATCAGAGACTGGATTTTCAACTCTTCTTAGAT 334
 QY 389 GAGGAACGGAGTAGGCTGTATGTGGAGCAAGGATCAATATTTTCACTGACCTGGTT 448
 DB 335 GAGGAAGAGGCGAGGCTGCTTGGAGCCAAAGACCATCTTTCTACTAGTCTGGTT 394
 QY 449 AA---TATCAAGGATTTTCAAAAGATTGTGTCGCGAGTATCTTACACCAAGAGATGAA 505
 DB 395 GACTTAAACAAAATTTTAAAGAGATTTATTGGCTGTGCAAGGACGGGTGGAATTA 454
 QY 506 TCAAGTGGGCTGGAAGAACATCTCTGAAAGAAATGTGCTAAATTTTCAAGTACTTAAG 565
 DB 455 TGTAATATTAGTGGGAAGATGCCAATACAGAAATGTGCAATTTTCACTAGACTTTCAG 514
 QY 566 GCATATAATCAGACTCACTGTGACGCTGTGGAACGGGGCTTTTTCATCCAAATTTGCACC 625
 DB 515 CCTATAACAAAACCTCACATATATGTGTGGAACCTGGAGCAATTTTCAATCAATATGTGG 574

QY 626 TACATTGAAATGGACATCATCCTGAGGACAATATTTTAAAGCTGGAGAACTCACAATTTT 685
Db 575 TATATTGATCTTTGGAGCTTCAAGGGGATATATATTCNAACTAGACACACATATTTTG 634
QY 686 GAAAACGGCGTGGGAAGAGTCCATATGACCCTAAGCTGCTGACAGCATCCCTTTTAATA 745
Db 635 GAGTCTGGCAGACTGAAATGTCTTCGATCCTCAGCAGCCTTTTGCTTCAGTAATGACA 694
QY 746 GATGGAGATTTATCTCGGAACCTCAGCTGATTTTATGGGGGAGACTTTGCTATCTTC 805
Db 695 GATGAGTACCTCTACTCTGGAACAGCTTCTGATTTCTTTGGCAAGATAGTGCATTCAC 754
QY 806 CGAACTCTTTGGGC-----ACCACCAACCAATCAGGACAGCAGCAGCATGATTCACGG 856
Db 755 CGATCCTTTGGGCCTACTCATGACCACCACTACATCAGAACTGACATTTTCAGAGCACTAC 814
QY 857 TGGCTCAATGATCCAAAGTTCATAGTGCACCTCACTCAGAGAGTGACAACTCCTGAA 916
Db 815 TGGCTCAATGGAGCAAAATTTATGGAACTTTCTTCATACCAGACACCTTACAATCCAGAT 874
QY 917 GATGACAAAGTATACCTTTTCTTCGTAAGAAATGCAATAGATGGAGAACACTCTCGAAAA 976
Db 875 GATGATAAATATATTTCTTTCTTCGTGATCATCTCAAGAGGCGAGTACCTCCGATAA 934
QY 977 GCTACTCAGCTAGATAGGTGAGATATGCAAGATAGCTTTGGAGGGGACAGAAAGCTG 1036
Db 935 ACCATCCTTTCTCGAGTTGGAAGAGTTTGTAAAGATGATGTAGAGGACAAACGACGCTG 994
QY 1037 GTGAATAAATGACAAACATTTCTCAAAGCTGCTGATTTGCTCAGTGCAGGTCCTCAAA 1096
Db 995 ATAAACAAGTGGACGACTTTCTTAAGGCCAGCTGATTTGCTCAATTCCTTGGAAAGTAT 1054
QY 1097 GGCATTGACACTCAITTTGATGAACCTGCAGAGTATTCCTAATGAACCTTTAAAGATCCT 1156
Db 1055 GGGGCAGATACCTTCTGATGAGCTTCAAGATATTTATTTACTCCCAACAGAGATGAA 1114
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Job time : 1260 secs

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OM nucleic - nucleic search, using sw model

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Gapop 10.0, Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2508.4	92.6	2601	1	US-08-835-268-53
3	2508.4	92.6	2601	3	US-09-060-692-53
4	2508.4	92.6	2601	3	US-08-833-391-53
5	2508.4	92.6	2601	4	US-09-060-610-53
6	2508.4	92.6	2601	5	PCT-US94-10151A-53
7	1415.2	52.2	1481	1	US-08-136-922-1
8	596.4	22.0	2898	4	US-09-308-179B-2
9	125	4.6	2278	4	US-09-976-594-1002
10	95.2	3.5	3692	4	US-09-077-940A-1
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30 58.4 2.2 3560 4 US-09-060-610-59 Sequence 59, Appl
31 58.4 2.2 3560 5 PCT-US94-10151A-59 Sequence 59, Appl
32 55.6 2.1 4286 4 US-09-976-594-632 Sequence 632, App
33 54.8 2.0 2504 1 US-08-121-713D-63 Sequence 63, Appl
34 54.8 2.0 2504 1 US-08-835-268-63 Sequence 63, Appl
35 54.8 2.0 2504 2 US-09-060-692-63 Sequence 63, Appl
36 54.8 2.0 2504 3 US-08-833-391-63 Sequence 63, Appl
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38 54.8 2.0 2504 5 PCT-US94-10151A-63 Sequence 63, Appl
39 54.6 2.0 2787 4 US-09-254-594-2 Sequence 2, Appl
40 54.6 2.0 3195 4 US-09-254-594-1 Sequence 1, Appl
41 48.6 1.8 2670 1 US-08-121-713D-61 Sequence 61, Appl
42 48.6 1.8 2670 1 US-08-835-268-61 Sequence 61, Appl
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44 48.6 1.8 2670 3 US-08-833-391-61 Sequence 61, Appl
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ALIGNMENTS

RESULT 1
US-08-121-713D-53
; Sequence 53 Application US/08121713D
; Patent No. 5639856
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713D
; FILING DATE: 13-SEP-1993
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..2331
US-08-121-713D-53
Query Match 92.6%; Score 2508.4; DB 1; Length 2601;
Best Local Similarity 100.0%; Pred. No. 0;

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Db 2169 GGATGAGTTCTGTGAACAGTTTGGAAAGGACCGAAAAACAACGTGCGCAAGGCCAGG 2228
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RESULT 2

US-08-835-268-53
; Sequence 53, Application US/08835268
; Patent No. 5807826
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matthes, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/835,268
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS

LOCATION: 16..2331
US-08-835-268-53

Query Match 92.6%; Score 2508.4; DB 1; Length 2601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 16..2331
US-09-060-692-53

Query Match 92.6%; Score 2508.4; DB 2; Length 2601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 1569 TATTTACGGGAAGCGTGTCTGAGTGTTCCTCGCCCGGAGACCTTACTGTCTGGGA 1628

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DB 1749 CAGCCCTGAAGAGAGATCATCTATGTTGTAGAGATAGTAGACATATTTTGGATGCGAG 1808

QY 1993 TCCGAAGTCCGAGAGAGCGCTGCTTATTTGGCAATTTCCAGAGCGGCAATGAAGAGCGAAA 2052
DB 1809 TCCGAAGTCCGAGAGAGCGCTGCTTATTTGGCAATTTCCAGAGCGGCAATGAAGAGCGAAA 1868

QY 2053 AGAAGAGATCAGAGTGGATGATCATCATCAGGACAGATCAAGGCTTCTGCTAGCTAG 2112
DB 1869 AGAAGAGATCAGAGTGGATGATCATCATCAGGACAGATCAAGGCTTCTGCTAGCTAG 1928

QY 2113 TCTAACACAGAAAGGATTCAGGCAATTTACCTCTGCCATGCGGTGGAAACATGGGTTTATACA 2172
DB 1929 TCTAACACAGAAAGGATTCAGGCAATTTACCTCTGCCATGCGGTGGAAACATGGGTTTATACA 1988

QY 2173 AACTCTTCTTAAGGTAACCTCGGAAGTCAATTGACACAGAGCATTTGGAGAACTTCTTCA 2232

Db 1989 AACTCTCTTTAAGGTAACCCCTGGAGTCAATGACACAGAGCAATTTGGAGAACTTCTTCA 2048
Qy 2233 TAAAGATGATGATGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAG 2292
Db 2049 TAAAGATGATGATGAGATGGCTCTAAGACCAAGAAATGTCCAATAGCATGACACCTAG 2108
Qy 2293 CCAGAAGTCTGTGTACAGAGACTTCATGAGCTCATCAACACCCCAATCTCAACAGAT 2352
Db 2109 CCAGAAGTCTGTGTACAGAGACTTCATGAGCTCATCAACACCCCAATCTCAACAGAT 2168
Qy 2353 GGATGAGTCTGTGAAACAATTTGGAAAGGGGCCGAAACCAACGTCGCGAAAGGCCAGG 2412
Db 2169 GGATGAGTCTGTGAAACAATTTGGAAAGGGGCCGAAACCAACGTCGCGAAAGGCCAGG 2228
Qy 2413 ACATACCCCGAGGACAGTACAAATGGAGCACTTACAGAAATAGAAAGGTAGAAA 2472
Db 2229 ACATACCCCGAGGACAGTACAAATGGAGCACTTACAGAAATAGAAAGGTAGAAA 2288
Qy 2473 CAGAGGACCCAGAAATTTGAGAGGGCACCCAGAGTGTCTGAGCTGCATTAACCTCTAGA 2532
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Qy 2533 AACCTCAAAACAAGTAGAAAATTCGCTAGACAATACTGGAAACCAAAATGCAATATACAT 2592
Db 2349 AACCTCAAAACAAGTAGAAAATTCGCTAGACAATACTGGAAACCAAAATGCAATATACAT 2408
Qy 2593 GAACTTTTTCATGGCAATATGAGATGTTTCAATGTTGAGGAAATTCAGCTGAGTTCCA 2652
Db 2409 GAACTTTTTCATGGCAATATGAGATGTTTCAATGTTGAGGAAATTCAGCTGAGTTCCA 2468
Qy 2653 CCAATTATAAATAAATCCATGAGTAACTTTCCTATAGCTTTTTC 2702
Db 2469 CCAATTATAAATAAATCCATGAGTAACTTTCCTATAGGCTTTTTC 2518

RESULT 4

US-08-833-391-53
; Sequence 53, Application US/08833391
; Patent No. 6013781
; GENERAL INFORMATION:
; APPLICANT: Goodman, Corey S.
; APPLICANT: Kolodkin, Alex L.
; APPLICANT: Matches, David
; APPLICANT: Bentley, David R.
; APPLICANT: O'Connor, Timothy
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 100
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
; STREET: 268 Bush Street, Suite 3200
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/833,391
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/121,713
; FILING DATE: 13-SEP-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Osgan, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415)343-4341
; TELEFAX: (415) 343-4342

TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16...2331
; US-08-833-391-53

Query Match 92.6%; Score 2508.4; DB 3; Length 2601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 193 CTGACGATGGGCTGGTTAACTAGGATGTCTCTTTCTGGGAGATTAATCTTACAGC 252
Db 9 CTGACGATGGGCTGGTTAACTAGGATGTCTCTTTCTGGGAGATTAATCTTACAGC 68
Qy 253 AAGACCAAACTATCAGAAATGGAAAGAAACAATGTGCCAAGGCTGAAATTTATCCCTACAAAGA 312
Db 69 AAGACCAAACTATCAGAAATGGAAAGAAACAATGTGCCAAGGCTGAAATTTATCCCTACAAAGA 128
Qy 313 AATGTTGGAATCCAAACAATGTGATCACTTTCAATGGCTTGGCCCAACAGCTCCAGTTATCA 372
Db 129 AATGTTGGAATCCAAACAATGTGATCACTTTCAATGGCTTGGCCCAACAGCTCCAGTTATCA 188
Qy 373 TACCTTCTCTTTGGATCAGGAACGGAGTAGGCTGTATGTGGAGCAAAAGATCACATATT 432
Db 189 TACCTTCTCTTTGGATCAGGAACGGAGTAGGCTGTATGTGGAGCAAAAGATCACATATT 248
Qy 433 TTCAATGCACTGGTTAATCAAGGATTTTCAAAAGATTTGTGGCCAGTAGTCTTTACAC 492
Db 249 TTCAATGCACTGGTTAATCAAGGATTTTCAAAAGATTTGTGGCCAGTAGTCTTTACAC 308
Qy 493 CAGAAGAGATGAATGCAAGTGGGCTGGAAAGACATCTTGAAGAATGTCTTAATTTTCAAT 552
Db 309 CAGAAGAGATGAATGCAAGTGGGCTGGAAAGACATCTTGAAGAATGTCTTAATTTTCAAT 368
Qy 553 CAAGTACTTAAGCATATAATCAGACTCACTTTGAGGCTGTGGACCGGGGCTTTTCA 612
Db 369 CAAGTACTTAAGCATATAATCAGACTCACTTTGAGGCTGTGGACCGGGGCTTTTCA 428
Qy 613 TCCAAATTTGCACTTACATTTGAATTTGGACATCATCTCTGAGGACAAATATTTTAAAGCTGA 672
Db 429 TCCAAATTTGCACTTACATTTGAATTTGGACATCATCTCTGAGGACAAATATTTTAAAGCTGA 488
Qy 673 GAATCAGATTTGAAAACGGCGGTGGAGAGTCCATATGACCTTACCTTACCTGACAGC 732
Db 489 GAATCAGATTTGAAAACGGCGGTGGAGAGTCCATATGACCTTACCTTACCTGACAGC 548
Qy 733 ATCCCTTTTATAGATGGAGAAATATATCTCTGAACTGCAGCTGATTTTATGGGCGAGA 792
Db 549 ATCCCTTTTATAGATGGAGAAATATATCTCTGAACTGCAGCTGATTTTATGGGCGAGA 608
Qy 793 CTTTGTCTATCTTCGAACTCTTGGGACACACCAATCAGACACGACAGCATGATTC 852
Db 609 CTTTGTCTATCTTCGAACTCTTGGGACACACCAATCAGACACGACAGCATGATTC 668
Qy 853 CAGTGGCTCAATGATCCAAAGTTCAATAGTGGCCACCTCATCTCAGAGAGTGACAATCC 912
Db 669 CAGTGGCTCAATGATCCAAAGTTCAATAGTGGCCACCTCATCTCAGAGAGTGACAATCC 728
Qy 913 TGAAGATGACAAAGTATACATTTTCTCGTGAATGCAATAGATGGAGAACACTCTGG 972
Db 729 TGAAGATGACAAAGTATACATTTTCTCGTGAATGCAATAGATGGAGAACACTCTGG 788
Qy 973 AAAAGCTACTCAGCTAGATAGGTGAGATATGCAAGAAATGCTTTGGAGGGGACAGAG 1032
Db 789 AAAAGCTACTCAGCTAGATAGGTGAGATATGCAAGAAATGCTTTGGAGGGGACAGAG 848


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; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: B94-002-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 343-4341
; TELEFAX: (415) 343-4342
; TELEX:
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..2331
; US-09-060-610-53

Query Match          92.6%; Score 2508.4; DB 4; Length 2601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 193 CTCAGCATGGGCTGTTAACTAGGATTGTCCTTTCTGGGAGATTACTTACAGC 252
Db 9 CTCAGCATGGGCTGTTAACTAGGATTGTCCTTTCTGGGAGATTACTTACAGC 68

QY 253 AAGAGCAAACTATCAGATGGGAAGAACAAATGTCGCAAGGCTGAAATTTATCCTACAAGA 312
Db 69 AAGAGCAAACTATCAGATGGGAAGAACAAATGTCGCAAGGCTGAAATTTATCCTACAAGA 128

QY 313 AATGTTGGAATCAACAATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCA 372
Db 129 AATGTTGGAATCAACAATGTGATCACTTTCAATGGCTTGGCCACAGCTCCAGTTATCA 188

QY 373 TACCTTCCTTTTGGATGAGGACGAGTAGGCTGTATGTTGGAGCAAGGATCACATATT 432
Db 189 TACCTTCCTTTTGGATGAGGACGAGTAGGCTGTATGTTGGAGCAAGGATCACATATT 248

QY 433 TTCAATTCGACCTGGTTAAATATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACAC 492
Db 249 TTCAATTCGACCTGGTTAAATATCAAGGATTTTCAAAAGATTTGTGGCCAGTATCTTACAC 308

QY 493 CAGAAGAGATGATCAAGTGGGCTGGAAAGACATCTGAAAGATGTGCTAATTTTCAAT 552
Db 309 CAGAAGAGATGATCAAGTGGGCTGGAAAGACATCTGAAAGATGTGCTAATTTTCAAT 368

QY 553 CAAGGTACTTAAGGCATATAATCAGACTCACTTTGACGCTGTGGAAAGGGGCTTTTCA 612
Db 369 CAAGGTACTTAAGGCATATAATCAGACTCACTTTGACGCTGTGGAAAGGGGCTTTTCA 428

QY 613 TCCAAATTTGACCTACATTTGAATTTGGAATTTGGAATTTGGAATTTTAAAGCTGGA 672
Db 429 TCCAAATTTGACCTACATTTGAATTTGGAATTTGGAATTTTAAAGCTGGA 488

QY 673 GAATCACTATTTGAAAACGGCCGTGGGAAGTCCATATGACCTAAGCTGTGACAGC 732
Db 489 GAATCACTATTTGAAAACGGCCGTGGGAAGTCCATATGACCTAAGCTGTGACAGC 548

QY 733 ATCCCTTTTAAATAGATGGAGAAATTAATCTCTGGAATCTGAGTATTTATGGGGCGAGA 792
Db 549 ATCCCTTTTAAATAGATGGAGAAATTAATCTCTGGAATCTGAGTATTTATGGGGCGAGA 608

QY 793 CTTTGTATCTTCCGAATCTTTGGGACACCAACCAATCAGGACAGAGCATGATTC 852
Db 609 CTTTGTATCTTCCGAATCTTTGGGACACCAACCAATCAGGACAGAGCATGATTC 668

QY 853 CAGTGGCTCAATGATCCAAAGTTCATTAGTCCCACTCATCTCAGAGAGTGACAAATCC 912
Db 669 CAGTGGCTCAATGATCCAAAGTTCATTAGTCCCACTCATCTCAGAGAGTGACAAATCC 728

QY 913 TGAAGATGACAAAGTATATCTTTTCTTCCGTGAAAATGCAATAGATGAGAACTCTGG 972
Db 729 TGAAGATGACAAAGTATATCTTTTCTTCCGTGAAAATGCAATAGATGAGAACTCTGG 788

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QY 973 AAAAGCTACTCAGCTAGAAATAGGTAGATATGCAAGAATGACTTTGGAGGGCACAGAAG 1032
Db 789 AAAAGCTACTCAGCTAGAAATAGGTAGATATGCAAGAATGACTTTGGAGGGCACAGAAG 848

QY 1033 TCTGTGTAATTAATGGACAAATTCCTCAAGAGCTGCTGATTTGCTCAGTGCAGGTCC 1092
Db 849 TCTGTGTAATTAATGGACAAATTCCTCAAGAGCTGCTGATTTGCTCAGTGCAGGTCC 908

QY 1093 AAATGGCAATTCACACTCATTTTGAATGAACCTGAGAGTATTCCTAATGAACCTTTAAAGA 1152
Db 909 AAATGGCAATTCACACTCATTTTGAATGAACCTGAGAGTATTCCTAATGAACCTTTAAAGA 968

QY 1153 TCCTAAAAATCCAGTTGTATATGAGAGTGTTCAGACTCCAGTAAACATTTTCAAGGATC 1212
Db 969 TCCTAAAAATCCAGTTGTATATGAGAGTGTTCAGACTCCAGTAAACATTTTCAAGGATC 1028

QY 1213 AGCCGTGTATGTATAGCATGATGTGAGAAGGCTGTCTCTGGTCCATATGCCCA 1272
Db 1029 AGCCGTGTATGTATAGCATGATGTGAGAAGGCTGTCTCTGGTCCATATGCCCA 1088

QY 1273 CAGGATGACACCAACTATCAATCGGTGCTTATCAAGGAAGAGTCCCTATCCAGGCC 1332
Db 1089 CAGGATGACACCAACTATCAATCGGTGCTTATCAAGGAAGAGTCCCTATCCAGGCC 1148

QY 1333 AGGAACTTGTCCAGCAAAACATTTGGTGGTGTGACTCTACAAAGGACCTTCTCTGATGA 1392
Db 1149 AGGAACTTGTCCAGCAAAACATTTGGTGGTGTGACTCTACAAAGGACCTTCTCTGATGA 1208

QY 1393 TGTATTAACCTTTGCAAGAGAGTCAATCAGGCATGTACATCCAGTGTTCCTATGACAA 1452
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QY 1453 TCGCCCAATAGTCAATCAAAACGAGTGTAAATATCAATTTACAAATTTGTCTGACACCG 1512
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QY 1513 AGTGAATGCAAGATGGAACAGTATGATTTATTCGGAACAGATTTGGGACCGT 1572
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QY 1873 AAGAAATGGAGACCACTGACTCACTGTTTACAGACTTTACCATGATATACCATGGCCA 1932
Db 1689 AAGAAATGGAGACCACTGACTCACTGTTTACAGACTTTACCATGATATACCATGGCCA 1748

QY 1933 CAGCCCTGAAGAGAGAAATCATCTATGTTAGAGAAATAGTAGACATTTTGGAAATGACAG 1992
Db 1749 CAGCCCTGAAGAGAGAAATCATCTATGTTAGAGAAATAGTAGACATTTTGGAAATGACAG 1808

QY 1993 TCCGAAGTTCGAGAGAGCGTGTGCTATTTGCAATTTCCAGAGCGGAAATGACAGAGGAAA 2052
Db 1809 TCCGAAGTTCGAGAGAGCGTGTGCTATTTGCAATTTCCAGAGCGGAAATGACAGAGGAAA 1868

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QY 2053 AGAAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTACGTAG 2112
Db 1869 AGAAGATCAGAGTGGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTACGTAG 1928
QY 2113 TCTACACAGAGGATTCAGGCAATTAACCTTGCCTGCGGTGGAACATGGGTTCATACA 2172
Db 1929 TCTACACAGAGGATTCAGGCAATTAACCTTGCCTGCGGTGGAACATGGGTTCATACA 1988
QY 2173 AACTCTTTTAAAGTAAACCTGGAAGTTCATTGACACAGAGCAATTTGGAAGAACTTCTTCA 2232
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QY 2233 TAAAGATGATGAGGATGGCTCTAAGACCAAGAAATGTCATATAGCATGACACCTAG 2292
Db 2049 TAAAGATGATGAGGATGGCTCTAAGACCAAGAAATGTCATATAGCATGACACCTAG 2108
QY 2293 CCAGAAGGTCTGTTACAGAGACTTCATGAGCTCATCAACCCCAATCTCAACACGAT 2352
Db 2109 CCAGAAGGTCTGTTACAGAGACTTCATGAGCTCATCAACCCCAATCTCAACACGAT 2168
QY 2353 GATGAGTCTCTGTAACAAAGTTTGGAAAGGACCGGAAACAACTGCGCAAGCCGAGG 2412
Db 2169 GATGAGTCTCTGTAACAAAGTTTGGAAAGGACCGGAAACAACTGCGCAAGCCGAGG 2228
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Db 2349 AACCTCAACAGTAGAAGTTCGCTAGACATACTGGAAGAAACAAATGCAATATACAT 2408
QY 2593 GAACCTTTTTCATGCAATTAATGAGTGTTCACAAATGTTGGAATTCAGCTGAGTTCCA 2652
Db 2409 GAACCTTTTTCATGCAATTAATGAGTGTTCACAAATGTTGGAATTCAGCTGAGTTCCA 2468
QY 2653 CCAATTATAATTAATCCATGAGTAATCTTCCTTAATAGGCTTTTTPCC 2702
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RESULT 6

PCT-US94-10151A-53
; Sequence 53, Application PC/TUS9410151A
; GENERAL INFORMATION:
; APPLICANT: The Regents of the University of California
; TITLE OF INVENTION: The Semaphorin Gene Family
; NUMBER OF SEQUENCES: 66
; CORRESPONDENCE ADDRESS:
; ADDRESS: FLHR HOBBACH TEST ALBRITTON & HERBERT
; STREET: 4 Embarcadero Center, Suite 3400
; City: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US94/10151A
; FILING DATE: 13-SEP-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Osman, Richard A.
; REGISTRATION NUMBER: 36,627
; REFERENCE/DOCKET NUMBER: PP-58750-PC/RAO
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299 FRI UR
; INFORMATION FOR SEQ ID NO: 53:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2601 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 16..2331
; PCT-US94-10151A-53
Query Match 92.6%; Score 2508.4; DB 5; Length 2601;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 2509; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
QY 193 CTGAGCATGGGTGTTAACTAGGATTGCTCTCTTTCTGGGGAGTATTACTTACAGC 252
Db 9 CTGAGCATGGGTGTTAACTAGGATTGCTCTCTTTCTGGGGAGTATTACTTACAGC 68
QY 253 AAGAGCAACTATCAGATCGGAGAAACAATGTGCCAAGGCTGAAATTTATCTTACAAAGA 312
Db 69 AAGAGCAACTATCAGATCGGAGAAACAATGTGCCAAGGCTGAAATTTATCTTACAAAGA 128
QY 313 AATGTTGGAATCCAAACAATGTGATCACTTTCAATGGCTTGGCCAAAGGATTTATCA 372
Db 129 AATGTTGGAATCCAAACAATGTGATCACTTTCAATGGCTTGGCCAAAGGATTTATCA 188
QY 373 TACCTTCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAGGATCACATATT 432
Db 189 TACCTTCTTTTGGATGAGGAACGGAGTAGGCTGTATGTTGGAGCAAGGATCACATATT 248
QY 433 TTCAATTCGACTCGTGTAAATTAATCAAGGATTTTCAAAAGATTTGTGCGCCAGTATCTAC 492
Db 249 TTCAATTCGACTCGTGTAAATTAATCAAGGATTTTCAAAAGATTTGTGCGCCAGTATCTAC 308
QY 493 CAGAAGAGATGAATGCAAGTGGGCTGGAAGACATCTGAAAGAAATGTCTAAATTTTCAT 552
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QY 553 CAAGGTACTTTAAGGCATATAATCAGACTCACTTTAGGCTGTGGAACGGGGCTTTTCA 612
Db 369 CAAGGTACTTTAAGGCATATAATCAGACTCACTTTAGGCTGTGGAACGGGGCTTTTCA 428
QY 613 TCCAAATTTGACCTCATTGAAATTCGACATCATCTGAGGACAAATATTTTAAAGCTGGA 672
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QY 673 GAACTCACATTTTGAAGACGGCGGTGGGAAGTCCATATGACCCCTAAGCTGCTGACAGC 732
Db 489 GAACTCACATTTTGAAGACGGCGGTGGGAAGTCCATATGACCCCTAAGCTGCTGACAGC 548
QY 733 ATCCCTTTTAAATAGATGGAGAAATTAACCTGGAAGTCCAGCTGATTTTATGGGGGAGA 792
Db 549 ATCCCTTTTAAATAGATGGAGAAATTAACCTGGAAGTCCAGCTGATTTTATGGGGGAGA 608
QY 793 CTTTGTCTATCTTCCGAACCTTTTGGGACCAACCCCAATCAGGACAGAGCAGCATGATTC 852
Db 609 CTTTGTCTATCTTCCGAACCTTTTGGGACCAACCCCAATCAGGACAGAGCAGCATGATTC 668
QY 853 CAGGTGGCTCAATGATCCAAAGTTCATTAGTGCACCACTCTCTCAGAGAGTGACATCC 912
Db 669 CAGGTGGCTCAATGATCCAAAGTTCATTAGTGCACCACTCTCTCAGAGAGTGACATCC 728
QY 913 TGAAGATGACAAAGTATATCTTTTCTTCGTGAAATGCAATAGATGGAACACTCTGG 972
Db 729 TGAAGATGACAAAGTATATCTTTTCTTCGTGAAATGCAATAGATGGAACACTCTGG 788
QY 973 AAAAGCTACTCAGCTAGATAGGTGAGATGCAATGCAAGTATGCTTTGAGGGGACAGAG 1032

TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-568-3100
TELEFAX: 215-568-3439
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1481 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: both
MOLECULE TYPE: cdna
FEATURE:
NAME/KEY: CDS
LOCATION: 50..1480
US-08-136-922-1

Query Match 52.2%; Score 1415.2; DB 1; Length 1481;
Best Local Similarity 99.4%; Pred. No. 0;
Matches 1420; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

QY 899 GAGAGTGCACATCTCGAAGATGACAAAGTATATCTTTCTTCGTTGAAATGCAATAGAT 958
DB 53 GAACATGACATCTCGAAGATGACAAAGTATATCTTTCTTCGTTGAAATGCAATAGAT 112
QY 959 GGAGAACACTCTGAAAAGCTTACTCAGCTAGATAGTTCAGATATCAAGAAATGACTTT 1018
DB 113 GGAGAACACTCTGAAAAGCTTACTCAGCTAGATAGTTCAGATATCAAGAAATGACTTT 172
QY 1019 GGAGGACAGAGTCTGGTGAATTAATGACACATCTCCTCAAGCTCTGCTGATTTGC 1078
DB 173 GGAGGACAGAGTCTGGTGAATTAATGACACATCTCCTCAAGCTCTGCTGATTTGC 232
QY 1079 TCAGTGCAGGTCCTCAATGTCATGACACTCAATTTGATCACTGCAGGATGATTTCTTA 1138
DB 233 TCAGTGCAGGTCCTCAATGTCATGACACTCAATTTGATCACTGCAGGATGATTTCTTA 292
QY 1139 ATGAATCTTAAAGATCTTAAATCCAGTTCATGATGAGTTCAGACTTCAGTTCCAGTAAC 1198
DB 293 ATGAATCTTAAAGATCTTAAATCCAGTTCATGATGAGTTCAGACTTCAGTTCCAGTAAC 352
QY 1199 ATTTTCAGGATCAGCGCTGTGTATGATGATGATGATGATGATGATGATGATGATGAT 1258
DB 353 ATTTTCAGGATCAGCGCTGTGTATGATGATGATGATGATGATGATGATGATGATGATGAT 412
QY 1259 GGTCCATATGCCAGGATGAGCCCAACTATCAATGGTGCCTTTATCAAGGAAGATC 1318
DB 413 GGTCCATATGCCAGGATGAGCCCAACTATCAATGGTGCCTTTATCAAGGAAGATC 472
QY 1319 CCCTATCCAGGACGAGGATCTGCCAGCAAAACATTTGGTGGTGGTGGTGGTGGTGGTGGTGG 1378
DB 473 CCCTATCCAGGACGAGGATCTGCCAGCAAAACATTTGGTGGTGGTGGTGGTGGTGGTGGTGG 532
QY 1379 GACCTTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1438
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QY 1499 ATTTGCTAGACGAGTGGATGACAGATGACAGATGATGATGATGATGATGATGATGATGATGAT 1558
DB 653 ATTTGCTAGACGAGTGGATGACAGATGACAGATGATGATGATGATGATGATGATGATGATGAT 712
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DB 773 GAGGTTCTGCTGGAGAAATGACAGTTCCTGGGACCGAGTCTGATTTTCAGCAATGGAG 832
QY 1679 CTTTCCACTAACGACCAACATATATATTTGTTCAACGGTGGGTTGCCAGTCCCT 1738

DB 833 CTTTCCACTAAGCAGCAACAACTATATATGGTTCAACGGCTGGGGTTGCCAGTCCCT 892
QY 1739 TTACACCGTGTGATATTTAGCGGAAGCGTGTGCTGAGTGTGCTGCTCGCCGAGACCT 1798
DB 893 TTACACCGTGTGATATTTAGCGGAAGCGTGTGCTGAGTGTGCTGCTCGCCGAGACCT 952
QY 1799 TACTGTGCTTGGGATGGTTCCTGCTATTTCTCGCTATTTTCCACTGCAAAAGAGACGACA 1859
DB 953 TACTGTGCTTGGGATGGTTCCTGCTATTTTCCACTGCAAAAGAGACGACA 1012
QY 1859 AGACGACAGATATTAAGAAATGGAGACCCACTGCTACTGTTTCCAGACTTACACCATGAT 1918
DB 1013 AGACGACAGATATTAAGAAATGGAGACCCACTGCTACTGTTTCCAGACTTACACCATGAT 1072
QY 1919 AATCACCATGGCCACAGCCCTCAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGCACA 1978
DB 1073 AATCACCATGGCCACAGCCCTCAAGAGAGAAATCATCTATGTTGTAGAGAAATAGTAGCACA 1132
QY 1979 TTTTGGATGACGTCGGAAGTCGAGAGAGCGCTGCTTATTTGCAATTTCCAGAGGCGA 2038
DB 1133 TTTTGGATGACGTCGGAAGTCGAGAGAGCGCTGCTTATTTGCAATTTCCAGAGGCGA 1192
QY 2039 AATGAGAGCGAAAGAGAGATCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 2098
DB 1193 AATGAGAGCGAAAGAGAGATCAGATGATGATGATGATGATGATGATGATGATGATGATGAT 1252
QY 2099 CTTTCTGCTACGTAAGTCTCAACAGAGAGATTCAGGCAATTTACCTCTGCCATCGGTGGAA 2158
DB 1253 CTTTCTGCTACGTAAGTCTCAACAGAGAGATTCAGGCAATTTACCTCTGCCATCGGTGGAA 1312
QY 2159 CATGGTTTCATCAAACTCTTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTA 2218
DB 1313 CATGGTTTCATCAAACTCTTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTAAGTTA 1372
QY 2219 GAAGAACTTCTTCATAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2278
DB 1373 GAAGAACTTCTTCATAAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1432
QY 2279 AGCATGACACCTAGCCAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2326
DB 1433 AGCATGACACCTAGCCAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1480

RESULT 8
US-09-308-1798-2
; Sequence 2, Application US/093081798
; Patent No. 6436669
; GENERAL INFORMATION:
; APPLICANT: INAGAKI, Shinobu
; APPLICANT: FURUYAMA, Tatsuo
; TITLE OF INVENTION: NOVEL SEMAPHORIN GENES (I)
; FILE REFERENCE: 0020-4562P
; CURRENT APPLICATION NUMBER: US/09/308,1798
; CURRENT FILING DATE: 1999-05-14
; PRIOR APPLICATION NUMBER: PCT/Jp97/04111
; PRIOR FILING DATE: 1997-11-12
; PRIOR APPLICATION NUMBER: JAPAN 321068/1996
; PRIOR FILING DATE: 1996-11-15
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 2898
; TYPE: DNA
; ORGANISM: Mus sp.
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2898)
; OTHER INFORMATION: Strandedness: Double-stranded
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(2898)
; OTHER INFORMATION: any n = a, c, g, t, unknown, or other
US-09-308-1798-2

Query Match		22.08; Score 596.4; DB 4; Length 2898;
Best Local Similarity		56.3; Pred. No. 4.5e-176;
Matches 1229; Conservative 0; Mismatches 911; Indels 24; Gaps 5;		
Qy	223	CTGTCTTTCTGGGGAGTATTACTATACAGCAAGAGCAAACTATCAGAAATGGGAAGAACAA 282
Db	396	CTTGCTCTCTGGGGTCACTGCTGGAACCTGGAACCCAGGTCATCTCGCGAACCCTC 455
Qy	283	TGTCGCAAGGCTGAAATATCTTACAAAGAAATGTTGGAATCCAAATGTGATCACTTT 342
Db	456	CTACCCAGGCTACGCTGTGCATATAAGAACTTTTGGAACTGAATAGGACTTCAATATT 515
Qy	343	CAATGGCTTGGCCAAACAGCTCCAGTTATCATCTTCTCTTGGATGAGGAACGGAGTAG 402
Db	516	TCAAAGCCCCCTTGGATTTCTTGNCTCCATACATGCTGCTGGATGAGTATCAAGAACG 575
Qy	403	GCTGTATGTTGGCAAGAGATCACATATTTTCAATTCGACCTGGTTAAATCA --- AGGA 459
Db	576	GCTCTTTTGGGGCAGAGACCTTGTCTATTCCCTGAACTTGGAAAGAGTCAAGTACGG 635
Qy	460	TTTTCAAGATTTGTGGCCAGTATCTTACACAGAGAGATGAATGCAAGTGGGCTCG 519
Db	636	CTACAGAGATATACCTGGCCGAGACACAGAGTAAGGTAGAAGATGCATATGAAGG 695
Qy	520	AAAGACATCTGAAAGATGTGCTAATTTTCATCAAGGTACTTTAAGGCATATAATCAGAC 579
Db	696	AAAAGA --- CGCAATGAGTGTGCCAATTATATCCGGGTTTTCATCACTACAACAGGAC 752
Qy	580	TCATTGTAGCCCTGGAGAGGGGCTTTTTCATCCAAATTTGCACCTACATTCGAATTCG 639
Db	753	ACACCTTCTGACCTGTCTACTGAGCTTTTGTATCCACACTGCTGCTTATCAGATCGG 812
Qy	640	ACATCATCTCTGAGACAATATTTTAACTGGAGAACTCACATTTTGAAGAACGGCCGCTG 699
Db	813	GCACCATTCAGAGAAACCCCTGTTTACCTGGAGTACACAGATCTGAGAGAGAGGG 872
Qy	700	GAGAGTCCATATGACCTTAAGCTGTGA CAGCATCCCTTTTAAATAGATGGAGAAATTA 759
Db	873	CAGATGTCCTTTTACCCCACTCCTCTTTGTGCCAGCTAGTTGGGAATGAGCTGT 932
Qy	760	CTCTGGAACCTGCAGCTCATTTTATGGGGCAGACTTTGTCTATCTTCGAACTCTCGGCA 819
Db	933	TGCTGGACTCTACAGTACTATTTGGGGCAGAGACTCGGCGAATTTTCGAGCATGGGAA 992
Qy	820	CCACCCCAATCAGGACAGCAGCATGATTCAGGTGGCTCAATGATCCAAAGTTTCA 879
Db	993	GTTAGGCCATATTCGCACCTGAGCATGACGATGAGCGCTCCTGAAAGAACCAAAATTTGT 1052
Qy	880	TAGTGGCCCACTCATCTCAGAGGTGACATCTCTGAGATGACAAAGTATATCTTTCTT 939
Db	1053	AGGTTTATATATGATTTCTGATACGAAGACCGAGATGACAAATAATGATCTTTTCTT 1112
Qy	940	CCGTGAAATTCGAATAGATGGAGAACACTCTGGAAGAGCTACTCAGCTAGAAATAGGTCA 999
Db	1113	TACTGAGAGGGCTGGAGCGGAGAACACGCCCAACAGATCTACACCGAGTGGGGG 1172
Qy	1000	GATATGAAGAAATGACTTTGGAGGGGACAGAGTCTGGTGAATTAATGACCAATCTCT 1059
Db	1173	GCTGTGGGTGAATGACATGGAGGACAGAGAACTCTGGTGAACAGAGTGGAGCACTTTCT 1232
Qy	1060	CAAGCTCGTCTGATTTGCTCAGTGGCCAGGTCCAAATGGCAATTCACATCTTTGATCA 1119
Db	1233	TAAAGCCGGCTGGTTTGTCTCAGTGGCGGAAATGAATGNAATCGACACATCTTTGACGA 1292
Qy	1120	ACTGAGGATGTATTCCTAATGAATTTAAAGATCTTAAAGATCCCAAGTTGTATATGAGT 1179
Db	1293	ACTAGGATGTGTTTTTACTGCGGACAGAGATCCCTAAGATCCCAAGTATTTGGACT 1352
Qy	1180	GTTTACGACTTCCAGTAACATTTTCAAGGATCAGCGCTGTGTATGTATAGCATGATGA 1239
Db	1353	GTTTAACTACAGCAATATATTTAGAGGCCATGCTGTATGTATGATCATCATGTCAAG 1412

Qy	1240	TGTGAGAGGGTGTCTTGTGTCATATGCCACAGGGATGGACCCAACTATCAATGGGT 1299
Db	1413	TATCCGGGAAGCCTTTAATGCCCATATGCTCATAAAGAGGCCCTGAATACCACGTGC 1472
Qy	1300	GCCTTATCAAGGAAGAGTCCCTATCCAGGCCAGGAACCTTGTCCAGCAAAACATTTGG 1359
Db	1473	ACTATATGAAGGAAAGTCCCTTACCAAGGCCCTGTCTGTGTGCCAGCAAGTAAACGG 1532
Qy	1360	TGG --- TTTTCACTCTCAAGAGGACCTTCTGTGATGATTTATTAACCTTTGCCAAGAATCA 1416
Db	1533	AGGCAAGTATGAACCAACCAAGATTACCCCGATGACGCCATCCGTTTCGAGGATGCA 1592
Qy	1417	TCCAGCCATGTACAATCCAGTGTTCCTATGAACAATGGCCCAATAGTATGATAAAGCGGA 1476
Db	1593	TCCTCTAATGTATCAGGCCATAAAACCTGTTTCAAAAAAACCAATACCTGTTAAAAACAGA 1652
Qy	1477	TGTAAATATCAATTTACAAATTTGCTGTAGACCGAGTGGATGCAGAGATGGACAGTA 1536
Db	1653	TGGAAATATCAACCTGAGGCAACTTGGCGTGGATCGGGTGGAGCGGAGATGGCCAGTA 1712
Qy	1537	TCATGTTATGTTTATCGGAAACAGATGTTGGACCGCTTCTTAAAGTAGTTCATTTCCATA 1596
Db	1713	TGACGTCTTATTTATTTGGACAGACACAGGAATTTGCTGAAAGTATATCAATTTACAA 1772
Qy	1597	GGAGACTTGTATGATTTTAGAGAGTTCCTGTGGAAGAAATGACAGTTCCTCGGAAACC 1656
Db	1773	CCAAGAAACAGAGTGGATGGAGGAAGTCACTTAGAGGAACTTCAAAATATTCAGAGTACC 1832
Qy	1657	GACTGCTATTTTCAACAATGGAGCTTCCACTAAGCAGCAACAATATATATTTGTTTCAAC 1716
Db	1833	AGCCCTATCATTTCTATGGAATTTCTTCAAGAGACACAGCTTTTACATTGATCAGC 1892
Qy	1717	GGCTGGGGTCCCGAGCTCCCTTTACACCGGTGTGATATTTACGGGAAAGCGTGTGCTGA 1776
Db	1893	CTCTGTGTGGCAACAAGTCAGATTCATCTGCGACATGATGGCAGTCTGTGTGCTGA 1952
Qy	1777	GTGTTGCTCCCGCAGACCTTACTGCTGTGGGATGGTTCTGCAATGTTCTCGCTATTT 1836
Db	1953	CTGTGCTGTGCTCGAGACCCGTAATGCTGCTGGGATGGCATATCTCTCTCCAGGTACTA 2012
Qy	1837	TCCACAC --- TGCAAAGAGACGCAACAAGACGCAAGAATATAAGAAATGGAGACC 1887
Db	2013	CCCAACAGGTGCACACACAAAGAGAGGTTCCCGCAGGACGACGTTCCGCATGSCAACGC 2072
Qy	1888	ACTGACTCAGTGTTCAGACTTACACATGATATCATCCATGGCCACAGCCCTGAGAGAG 1947
Db	2073	CGCCCAACAGTGTCTTTGGACAGCAATTTGTTGGAGACGCGTTGGACAGGACTGAAGAG 2132
Qy	1948	AATCATCTATGCTGTAGAGAAATAGTACATATTTTGGAAATGCACTCCGAAGTCGCAGAG 2007
Db	2133	GCTGGCTTATGCGATAGAGACACAGTACTCTGTTGGAATGACCCCGCGATCACTACA 2192
Qy	2008	AGCGTGGTCTATTGGCAATTCAGAGCGGAAATGAAGAGCGAAAGAGAGATCAGAGT 2067
Db	2193	AGCAAAAGTCTACTCTGGTTGTACAGAAAGGACGCGACGTAAGAAAGAGAGGTTGAAGAC 2252
Qy	2068	GGATGATCATATCATCAGGACAGATCAAGGCTTCTGCTACGTAGTCTCAACAAGAGGA 2127
Db	2253	GGATGACAGAGTGTGTAAGATGAGTCTGCTCTTCTCCTCAGATGACAGTACAGT 2312
Qy	2128	TTGAGGCAATTAACCTCTGCCATCGGTTGGAACATGAGGTTTATCAAAACTCTTCTTAAGT 2187
Db	2313	TGAGGACCTTATTTTGGCAGACAGTAGAACAAATTTTGTCCATCTCTGCTGCTGCTTAAAT 2372
Qy	2188	AACCTTGGAGTCAATTCACAGAGCATTTGGAGAACTTCTTCAATGAAGATGATGATG- 2246
Db	2373	CACCTTGGAGTGTGTCGAAGAGCATAAAGTGGAGGGCATGTTTTCATGAAGACCATGAAGA 2432
Qy	2247	-----GAGATGGCTCTTAAGACCAAGAAATGTCCAATAGCATGACACTAGCCAGGAAGGT 2301
Db	2433	GGAAAGACATCAAGAATGCCCTCCCTTAAAGCGGTATGTTCTCAGGGGACAAAACC 2492
Qy	2302	CTGCTACAGAGACTTCATGAGCTCATCAACCCCACTCAACAGCATGGATGAGTT 2361

Db 2493 GTGGTACAGGAATCTTGTGAGCTGATGGCTACAGCAATCTCCAGAGAGTGAAGAATA 2552
 QY 2362 CTGTGAACAAAGTTTGGAAAAGGGA 2385
 Db 2553 CTGCGAAAAGTGTGGTGTACAGA 2576

RESULT 9
 US-09-976-594-1002
 ; Sequence 1002. Application US/09976594
 ; Patent No. 6673549
 ; GENERAL INFORMATION:
 ; APPLICANT: Furness, Michael
 ; APPLICANT: Buchbinder, Jenny
 ; TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
 ; FILE REFERENCE: PA-0041 US
 ; CURRENT APPLICATION NUMBER: US/09/976,594
 ; CURRENT FILING DATE: 2001-10-12
 ; PRIOR APPLICATION NUMBER: 60/240,409
 ; PRIOR FILING DATE: 2000-10-12
 ; NUMBER OF SEQ ID NOS: 1143
 ; SOFTWARE: PERL Program
 ; SEQ ID NO 1002
 ; LENGTH: 2278
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: misc feature
 ; OTHER INFORMATION: Incyte ID No. 6673549 411373.7
 US-09-976-594-1002

Query Match 4.6%; Score 125; DB 4; Length 2278;
 Best Local Similarity 50.5%; Pred. No. 2.2e-28;
 Matches 488; Conservative 0; Mismatches 440; Indels 39; Gaps 6;

QY 689 AACGGCCGTGGGAAGAGTCCATATGACCCTAAGCTGTGACAGCATCCCTTTTAATAGAT 748
 Db 758 AGCGAATGCCAGATGCCATATGATGCCAAACATGCCAACCTTGACCTGTTGTCAGAT 817
 QY 749 GGAGAAATTAATCTGGAACATGACATGATTTATGGGGGAGACTTGTCTATCTCCGA 808
 Db 818 GGAATACTATACTAGCCACAGTGAATGCTTCTTCCATGACGAGCATTTTACCGG 877
 QY 809 ACTCTTGGGACACCCACCAATCAGGACAGAGATGATTCAGGTGGCTCAATGAT 868
 Db 878 AGCTTTGGAGAAGCCCTACCTCGGACCGTCAAGCAGATTCAAATGGTTGAAGAA 937
 QY 869 CAAAGTTTCAATGAGCCCACTCATCTCAGAGATGACAATCTCGAAGATGACAAAGTA 928
 Db 938 CCATATCTTGTTCAGGCGGTGA-----TTACGGAGATTATATC 976
 QY 929 TACTTTTCTCCGTGAATGCAATAGATGAGAGAACTCTGGAAGAGTACTCAGCT 988
 Db 977 TACTTCTCTTCAGGGAATAGCAGTGGAGTATACACCATGGGAAGGTAGTTTCCCA 1036
 QY 989 AGAATAGTTCAGATATGCAAGAAATGACTTTGGAGG---GCACAGAGTCTGGTAATAA 1045
 Db 1037 AGAGTGGCTCAGTTTGTGAAGAATGATATGGAGGATCTCAAAGAGTCTCGAGAAACAG 1096
 QY 1046 TGGACAACTTCTCAAGCTCGTCTGATTTGCTCAGTGCCAGGTCCTCAATGGGATTCAC 1105
 Db 1097 TGGACGCTCTTCTCAAGCGCGCTTGAAGTCTCAGTCTCTGG-----AGACTCTCAT 1150
 QY 1106 ACTCATTTTGTGAATGAGTGCAGATGATTTCTTAATGAATCTTAAAGATCTTAAATAATCCA 1165
 Db 1151 TTTTATTTCACATCTCCAGGAGTTACAGATGATGATTCGATATCAACGGGCGTAT--- 1207
 QY 1166 GTTGTATATGAGAGTGTTCAGACTTCCAGATATCAATTTTCAAGGATTCAGCGGTGTATG 1225
 Db 1208 GTTGTCTTGGCAACGTTTCTACACTTATACAGCATCTCCCTGGGTCTCGACTCTGTGCC 1267
 QY 1226 TATAGCATGATGTGAGAGGGTGTTCCTTGTGTCCATATGCCCCACAGGATGGACCC 1285

Db 1268 TATGATCTGCTTGACATTCGAGTGTCTTCTTACTGGAGATTCAAGGAACAGAGTCTCCT 1327
 QY 1286 AACTATCAATGGGTGCC---TTATCAAGGAAGAGTCCCTATCCACGCCGAGGACTTGT 1342
 Db 1328 GATTCACCTGGACACACAGTTCCTGATGACAGAGTCTTAAGCCGAGGCCAGGTGCTGT 1387
 QY 1343 CCCAGCAAA---ACATTTGGTGGTTTGACTCTACAAAGGACCTTCTCTGATGATTTATA 1399
 Db 1388 GCTGGCTCATCTCTCTTGAAGAAGATGCAACCTCCATGATGATTCCTGATGATACCTGT 1447
 QY 1400 ACCTTTGAAGAAGTCAATCCAGCCATGATCAATCCAGTGTTCCTATGAACAAATGCCCA 1459
 Db 1448 AACTTTCATCAAGACGACCCGCTCATGATGATGAGGAGTCCCTCATCTTCAACAGGCCA 1507
 QY 1460 ATAGTATGATCAAAACGATGTAATATCAATTTACACAAATTTGCTAGACCGAGTGGAT 1519
 Db 1508 TGGTTCCTGAGAAACAATGTCAGATCCGCTTACCAAAATTTGAGTGGACACACTGCT 1567
 QY 1520 GCAGAAGATGACAGATGATGATTTATGTTATCGAAACAGATGTTGGACCGTCTTTAAA 1579
 Db 1568 GGGCCATATCAGATCAGACTGTGTTTCTGGGATCAGAGAGGGAATCATCTTGAAG 1627
 QY 1580 GTAGTTTCAATTCCTAAGAGACTTGGTATGATTTAGAGAGGTTCTCTGGAAGAAATG 1639
 Db 1628 TTTTGGCCAGAAATAGTAATAGTGTGTTTCTTAATGACAGCCTTTTCTGGAGGAGATG 1687
 QY 1640 ACAGTTT 1646
 Db 1688 AGTGTTT 1694

RESULT 10
 US-09-077-940A-1
 ; Sequence 1. Application US/09077940A
 ; Patent No. 6576441
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMURA, Toru et al.
 ; TITLE OF INVENTION: NOVEL SEMAPHORIN 2 AND GENE ENCODING THE SAME
 ; FILE REFERENCE: 0020-4426P
 ; CURRENT APPLICATION NUMBER: US/09/077,940A
 ; CURRENT FILING DATE: 1998-06-05
 ; NUMBER OF SEQ ID NOS: 20
 ; SOFTWARE: Patent in version 3.1
 ; SEQ ID NO 1
 ; LENGTH: 3692
 ; TYPE: DNA
 ; ORGANISM: Rattus norvegicus
 ; FEATURE:
 ; NAME/KEY: 5'UTR
 ; LOCATION: (1)..(18)
 ; OTHER INFORMATION:
 ; NAME/KEY: CDS
 ; LOCATION: (19)..(2682)
 ; OTHER INFORMATION:
 ; NAME/KEY: 3'UTR
 ; LOCATION: (2683)..(3653)
 ; OTHER INFORMATION:
 ; NAME/KEY: PolyA_site
 ; LOCATION: (3654)..(3692)
 ; OTHER INFORMATION:
 ; US-09-077-940A-1

Query Match 3.5%; Score 95.2; DB 4; Length 3692;
 Best Local Similarity 47.8%; Pred. No. 6.7e-19;
 Matches 431; Conservative 0; Mismatches 438; Indels 33; Gaps 4;

QY 705 GTCCATATGACCTTAAGCTGCTGACAGCATCCCTTTTAATAGATGAGAAATTATCTCTG 764
 Db 542 GCCCTACGACCCCAAGCATGCCAATGTCGCCCTCTTCTCAGATGGATGCTCTTCCACAG 601
 QY 765 GAATGAGCTGATTTTATGGGGGAGACTTTCGTATCTTCGAACTCTTGGGCACACC 824

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602 CCACGTAACGACTTCTAGCCATCGACGCTGTTATCTACCGTAGCTTTGGGACCGGC 661
QY ACCCAATCAGACAGACAGATGATTCAGGTGGCTCAATGATCCAAAGTTCATGATG 894
Db CCACACTCGCACAGTAAAGCATGACTCCAAGTGGTTTAAAGAGCCCATCTTTGTCATG 721
QY CCCACCTCATCTCAGAGAGTGACAATCCTGAAGATGACAAAGATATCTTTTCTTCGCTG 944
Db CGGTGGAGTGGGAG-----CCAGTCTACTTCTTCTTCGGG 760
QY AAAATGCAATAGATGGAGAACACTCTCGAAAGACTACTCAGCTAGATAGGTGAGATAT 1004
Db AGATCGCCATGGAGTTAACTATCTGGAAGAGTGGTGGTCTCCGCTGTCGCGCGTGTAT 820
QY GCAGAGATGACTTTGGAGGACACAGAG---TCTGGTGAATAAATGACACAACTTCTCTCA 1061
Db GCAAGATGATGTGGCGGCTCCCGGCTGCTGGAGAGCAGTGGACTTCTTCTCTGA 880
QY AAGCTCGTCTGATTTGCTCAGTGCAGGTCCAAATGGCATTGACACTCACTTTTGAAGAC 1121
Db AGGCCCGCTCAACTGCTCGTGGCTGG-----GGACTCACACTTCTACTTCAATGTAC 934
QY TGCAGGATGATTCCTAATGACTTTAAGATCTTAAATTCAGTTGATGATGATGATGATG 1181
Db TGCAGGCTGTGACTGGTGTG---GTGAGCCTTGGCGCGCTCCAGTGAATCTTTGCTGTCT 991
QY TTACGACTTCCAGTAACATTTTCAAGGATCAGCGGTGTGTATGATAGCATGAGTATG 1241
Db TCTCAATCTCTAGCAAGCATCCCTGGCTCAGCTGTCTGTGCTTTGACATGACCAAG 1051
QY TGAGAGGGGTCTCTTGGTCCATATGCCACAGGAGTGAACCCAACTATCAATGGGTGC 1301
Db TGGCTGTGTGTTTGAAGGCGCTTCCGGGAGCAGAGTCACTGAGTCAATCTGGACCC 1111
QY CTTATCAAGAGAGTCCCTATCCAGCGCCAGGAATCTTCCAGCAAAACATTTGGTG 1361
Db CAGTGCCTGAGGACCAAGTACAGCGCCAGGCGCGGTCTGTGAGCGCCCGGTATGC 1171
QY GTTTTGACTCTCAAGAGACTTCTCTGATGATGTTATTAACCTTTGCAAGAGTCAATCCAG 1421
Db AGTCAACGCAATCAATGCTGCTCTGACGAGATTTCTCACTTTGTAAGACCCACCCAC 1231
QY CCATGTACATCCAGTGTCTTCTATGAAATGCAATGCCCAATAGTATGATCAAAACGATGTA 1481
Db TGATGGAGAGAGCGGTGCCCTCCCTGGGCCACTCGCCCTTGGATTTGTGAGAACTTCTGATAC 1291
QY ATTATCAATTTACAAATTTGTGTAGACGAGTGGATGAGAGATGAGACAGTATGATG 1541
Db GGCACCACTGACCGAGTGGCTGTGATGATGGGTGAGGCCCATCGGCAATCAGACAA 1351
QY TTATGTTTATCGAGACAGATGTTGGGACCGTCTTTAAAGTATGTTTCAATCTTCAAGGAGA 1601
Db TAGTCTTCTTGGCTCTGAGGTTGGACAGTCTCTCAATTTCTTGTGAAGCCCAATGGCA 1411
QY 1602 CT 1603
Db 1412 GT 1413

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RESULT 11

US-09-653-274-12
Sequence 12, Application US/09653274
Patent No. 6635742
GENERAL INFORMATION:

APPLICANT: Boyle, Bryan J
APPLICANT: Yeung, George Y
APPLICANT: Arterburn, Matthew C
APPLICANT: Mize, Nancy K
APPLICANT: Tang, Y. Tom
APPLICANT: Liu, Chenghua
APPLICANT: Drmanac, Radoje T
TITLE OF INVENTION: Methods and Materials Relating to Semaphorin-Like
TITLE OF INVENTION: Polypeptides and Polynucleotides

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FILE REFERENCE: HVS-23
CURRENT APPLICATION NUMBER: US/09/653,274
CURRENT FILING DATE: 2000-08-31
PRIOR APPLICATION NUMBER: 09/491,404
PRIOR FILING DATE: 2000-01-10
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 12
LENGTH: 1923
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)..(1923)
US-09-653-274-12

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Query Match 3.3%; Score 90.6; DB 4; Length 1923;
Best Local Similarity 49.0%; Pred. No. 1.2e-17;
Matches 444; Conservative 0; Mismatches 424; Indels 39; Gaps 6;
QY 692 GCGCTGGGAAGAGTCCATATGACCCCTAAGCTGCTGACAGCATCCCTTTTAAATAGATGGA 751
Db 436 GCGCTGGCAAGATGCCCATTTGATGCCAGACAAACCAATGTTGCCCTTTTGTGCTGATGG 495
QY 752 GAATTTATCTCTGAACTGTCAGCTGATTTTATGGGCGAGACTTTTGTCTATCTTCCGAAC 811
Db 496 AAGCTGTATTCTGCCACAGTGGCTGACTTCTTGGCCAGCGATGCCGTTATTTATCGAAGC 555
QY 812 CTGGGCAACACCCCAATCAGACAGACAGATGATTCAGGTGGCTGCTCAATGATCCA 871
Db 556 ATGGGTGATGATGTGCCCTTCGCACAAATAATATGATTTCCAAATGATAAAGAGCCA 615
QY 872 AAGTTCAATAGTGGCCCACTCATCTCAGAGAGTGAACAATCCTGAAGATGACAAAGATATAC 931
Db 616 CACTTCTTCATGC-----CATAGAATATGGAACATATGCTAT 654
QY 932 TTTTCTTCCTGGAATGCAATAGATGGAGAACACTCTGGAAGACTACTCAGCTAGA 991
Db 655 TTTCTTTTCAGAAATGCGTGTGCGAACATAATTAATTTAGCAAGGTGTGTTATTCGCG 714
QY 992 ATAGTTCAGATATGCAAGATGACTTTGGAGGG---CACAGAGTCTGGTGAATAAATGG 1048
Db 715 GTGGCCCGCATATGTAAAGACGACATGGGTGTTCCAGCGGGTCTGGAGAACACTGG 774
QY 1049 ACAACATTCCTCAAGCTGCTGCTGATTTGCTCAGTGCAGGTCCAAATGCGATTTGACACT 1108
Db 775 ACTTCATTTCAAAGGGTTCGGCTGAACTGTTCTGCTCGAGATCCGTTTTTCTAC--- 831
QY 1109 CATTTGATGAATGTCAGGATGATTTCTTAATGAACCTTTAAAGATCTTAAATTTCCAGTT 1168
Db 832 ---TTTGATGTTCTGAGTCTATTACAGACATA---TACAAATCAATGCAATCCCACT 885
QY 1169 GTATATGAGTGTTTACGACTTCCAGTAACATTTTCAAGGATCAGCGGTGTGTATGATAT 1228
Db 886 GTGGTCGGGGTGTTTTACACGACGCTCAATAGCATCCCTGTTCTGCTGTCTGTGCTATTT 945
QY 1229 AGCATGATGATGTGAGAGGGTTCCTTGGTCCATATGCCACAGGATGGACCCCAAC 1288
Db 946 AGCATGATGATGTGAGAGGGTTCCTTGGTCCATATGCCACAGGATGGACCCCAAC 1005
QY 1289 TATCAATGGGTGCTTATC---AAGGAGAGTTCCTTATCCAGCGCCAGGAACCTTTGCC 1345
Db 1006 TCTGTTGGACAGCAGTTCCCGAAGACAAAGTGCACAAAGCAAGGCTGTGCTGTTGTGCA 1065
QY 1346 AGCAAAACATTT---GGTGGTTTGTACTCTACAAGAGACCTTCTGTATGATGATTAACC 1402
Db 1066 AAACACGCGCTTGGCGAAGCTTATAAAACCTCCATGATTTCCCGGATGAACCTCTGTCA 1125
QY 1403 TTTGCAAGAGTCAATCCAGCCATGTAACAATCCAGTGTTCCTATGAACAATCGCCCAATA 1462
Db 1126 TTCAATAATCTCATCCCTGATGAGTCTGCGGTTCACCCCATGCGGATGAGCCCTGG 1185
QY 1463 GTGATCAAAACGAGTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 1522

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Db 1186 TTCAAAAGACTCGGTTCAGTACAGACTGACGGCCATCTCAGTGGACCACTTTCAGCCGGA 1245
 QY 1523 GAAGATGGACAGTATGATGTTATGTTATCGGAACAGATGTTGGACCGGTTCTTAAAGTA 1582
 Db 1246 CCCTACAGAACTACACAGTCACTCTTGTGGCTCTGAGCTGGCATGGTACTTAAAGTT 1305
 QY 1583 GTTTCAA 1589
 Db 1306 CTGGCAA 1312

RESULT 12

US-09-653-274-5
 ; Sequence 5, Application US/09653274
 ; Patent No. 6635742
 ; GENERAL INFORMATION:
 ; APPLICANT: Boyle, Bryan J
 ; APPLICANT: Yeung, George Y
 ; APPLICANT: Arterburn, Matthew C
 ; APPLICANT: Mize, Nancy K
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Dmanac, Radoje T
 ; TITLE OF INVENTION: Methods and Materials Relating to Semaphorin-Like
 ; TITLE OF INVENTION: Polypeptides and Polynucleotides
 ; FILE REFERENCE: HYS-23
 ; CURRENT APPLICATION NUMBER: US/09/653,274
 ; CURRENT FILING DATE: 2000-08-31
 ; PRIOR FILING DATE: 2000-01-10
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 5
 ; LENGTH: 3261
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 US-09-653-274-5

Query Match 3.3%; Score 90.6; DB 4; Length 3261;
 Best Local Similarity 49.0%; Pred. No. 1.7e-17;
 Matches 444; Conservative 0; Mismatches 424; Indels 39; Gaps 6;
 QY 692 GGCGTGGGAAGTCCATATGACCCCTAAGTGTGACAGATCCCTTTTAAATAGTGA 751
 Db 484 GGCGTGGGAAGTCCATATGACCCCTAAGTGTGACAGATCCCTTTTAAATAGTGG 543
 QY 752 GAATTTATCTCTGGAACCTGACGCTGATTTTATGGGGGAGACTTGTCTATCTCCGAACT 811
 Db 544 AAGCTGATTTCTGCCAGTGGCTGACTTCTTGGCCAGCATGCCGTTATTTATCGAAGC 603
 QY 812 CTGGGCAACCAACCCCAATCAGACAGAGATGATCCAGGTGGCTCAATGATCCA 871
 Db 604 ATGGTGTGATGATCTGCGCTTCGCACATAAATATGATTTCCAAATGGATAAAGAGCCA 663
 QY 872 AAGTTCATTAGTGGCCCACTCATCTCAGAGATGACATCTGAGATGACAAAGTATAC 931
 Db 684 CACTTCTTCATGC-----CATGAATATGAACTATGCTAT 702
 QY 932 TTTTCTTTCCTGGAATATGCAATAGAGGAGAACACTCTGGAAGAGTACTCAGCGTGA 991
 Db 703 TTTCTTCTTCGGAATATGCTGTGCAACATAATATTTAGCAAGGCTGTGATTTCCCGC 762
 QY 992 ATAGTTCAGATATGCAAGATGACTTTGGAGG---CACAGAAGTCTGGTAATAATGG 1048
 Db 763 GTGGCCCGCATATGTAAGAACAGACATGGGTGTTCCAGCGGGTCTGGAGAACACTGG 822
 QY 1049 ACAACATTCCTCAAGCTCGTCTGATTTTGTCTCAGTGGCCAGGTCCAAATGGCAATGACACT 1108
 Db 823 ACTTCATTTCTAAGGCTCGGCTGACTGTTCTGCTCCCTGGAGATCCGTTTTTCTAC--- 879
 QY 1109 CATTGTTGATGAACTCGAGATGATTTCTCTAATGAACCTTTAAGATCTTAAATCCAGTT 1168

Db 880 ---TTTGATGTTTCTGAGTCTATTATACAGACATAA---TACAAATCAATGGCATCCCCACT 933
 QY 1169 GTATATGAGTGTGTTTACGACTTCCAGTAAACATTTTCAAGGGATCAGCGTGTGTATGAT 1228
 Db 934 GTGGCGGGGTGTTTACCAAGAGCTCAATAGCATCCCTGGTTCGTCTGTCTGTGCAATT 993
 QY 1229 AGCATGAGTGTGAGAAAGGTGTTCTTGTTCATATGCCCAAGGATGGACCCCAAC 1288
 Db 994 AGCATGGATGACATTTGAAAGAGTATTCAAGAGACGGTTTAAAGGAACAGAAATCTCCAGAT 1053
 QY 1289 TATCAATGGTGCCTTATC---AAGGAAGAGTCCCTATCCAGGCCAGGAACCTTGTCCC 1345
 Db 1054 TCTGTTTGGACAGAGTTCCTCCGAGACAAAGTCCCAAGCCCTGGCTGTGTGCA 1113
 QY 1346 AGCAAAACATTT---GGTGGTTTTGACTCTACAAAGGACCTTCTCTGATGATGTTATAACC 1402
 Db 1114 AAACACGGCTTGGCGAAGCTTTATAAACCTCCATCGATTTCCCGGATGAAACTCTGTCA 1173
 QY 1403 TTTGCAAGNAGTCAATCCAGCCATGACAAATCCAGTGTTCCTATGAAACAATGCCCAATA 1462
 Db 1174 TTTATCAAAATCTCATCCCTGATGACTCTGCGTTCCACCAATGCGGATGAGCCCTGG 1233
 QY 1463 GTGATCAAAACGGATGTAATTTATCAATTTACAAATTTCTGTAGACCGAGTGGATGCA 1522
 Db 1234 TTCAAAAGACTCGGTTCAGGTACAGACTGACGGCCATCTCAGTGGACCACTTTCAGCCGGA 1293
 QY 1523 GAAGATGGACATGATGATGTTTATCGGAACAGATGTTGGACCGTCTTCTTAAAGTA 1582
 Db 1294 CCTACCAAGACTACACAGTCACTTTTGTGGCTCTGAAAGCTGGCATGGTACTTAAAGTT 1353
 QY 1583 GTTTCAA 1589
 Db 1354 CTGGCAA 1360

RESULT 13

US-09-653-274-3
 ; Sequence 3, Application US/09653274
 ; Patent No. 6635742
 ; GENERAL INFORMATION:
 ; APPLICANT: Boyle, Bryan J
 ; APPLICANT: Yeung, George Y
 ; APPLICANT: Arterburn, Matthew C
 ; APPLICANT: Mize, Nancy K
 ; APPLICANT: Tang, Y. Tom
 ; APPLICANT: Liu, Chenghua
 ; APPLICANT: Dmanac, Radoje T
 ; TITLE OF INVENTION: Methods and Materials Relating to Semaphorin-Like
 ; TITLE OF INVENTION: Polypeptides and Polynucleotides
 ; FILE REFERENCE: HYS-23
 ; CURRENT APPLICATION NUMBER: US/09/653,274
 ; CURRENT FILING DATE: 2000-08-31
 ; PRIOR FILING DATE: 2000-01-10
 ; NUMBER OF SEQ ID NOS: 13
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 3
 ; LENGTH: 3694
 ; TYPE: DNA
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (434) .. (3694)
 US-09-653-274-3

Query Match 3.3%; Score 90.6; DB 4; Length 3694;
 Best Local Similarity 49.0%; Pred. No. 1.8e-17;
 Matches 444; Conservative 0; Mismatches 424; Indels 39; Gaps 6;
 QY 692 GGCGTGGGAAGTCCATATGACCCCTAAGTGTGACAGATCCCTTTTAAATAGTGA 751
 Db 917 GGCGTGGGAAGTCCATATGACCCCTAAGTGTGACAGAACCAATGTTGCCCTCTTTGCTGATGGG 976

752 GAATTTACTCTGGAAGTCTGAGTCTGATTTTATGGGCGAGACTTTGCTATCTTTCCGAAT 811
 Db AAGCTGTATTCTGCCAGTGGCTGACTTCTTCTGCCAGGATCGCGTTTATTTATCGAAGC 1036
 Qy 812 CTTGGGACCAACCACCAATCAGGACGAGCAGATGATTCAGGTGGCTCAATGATCA 871
 Db 1037 ATGGGTGATGATCTGGCTTCGCACAAATAAATATGATTCCAAATGGATAAAGAGCCA 1096
 Qy 872 AAGTTCAATAGTGGCCACCTCATCTCAGAGAGTGACAAATCCTGAAGATGACAAAGTATAC 931
 Db 1097 CACTTTCTTCATG-----CATGAATATGGAACATATGCTAT 1135
 Qy 932 TTTTCTTCCTGGAATGCAATAGATGGAGACACCTCTGGAAAAGCTACTCAGGTAGA 991
 Db 1136 TTCTTTCTTCGAGAAATCGCTGCAACATAAATTTAGSCAAGCTGTGTATTCCTCCG 1195
 Qy 992 ATAGTTCAGATATGCAAGATGACTTTTGGAGG--CACAGAAGTCTGTGTAATAATGG 1048
 Db 1196 GTGCCCGCATATGTAAGAACGACATGGGTGTTCCAGCGGTCTGGAGAACACTGG 1255
 Qy 1049 ACACATTTCTCAAGCTCTGATTTGCTCAGTCCAGGTCCAAATGGCAATGACAT 1108
 Db 1256 ACTTCAATTTCAAAGCTCGCTGAACTGTTCTGCTCCAGATCGGTTTCTTCTAC--- 1312
 Qy 1109 CATTTGATGACTGCAAGATGATTCCTTAATGAATTTAAAGATCCTTAAATCCAGTT 1168
 Db 1313 ---TTTGATGTTCTGCACTCTATTACAGACATAA---TACAAATCAATGGCATCCCACT 1366
 Qy 1169 GTATATGAGTGTATTACGACTTCCAGTAACATTTTCAAGGGATCAGCGGTGTATGAT 1228
 Db 1367 GTGTGCGGGTGTATTACGACAGCTCAATAGCATCCCTGTTCTGCTGTGTCATTT 1426
 Qy 1229 AGCATGATGATGAGAGGGGTGTTCTTGTGTCATATGCCACAGGATGAGACCCAC 1288
 Db 1427 AGCATGATGACATTTGAAAGATTTTCAAAGGACGGTTTAAAGAACAGAAACTCCAGAT 1486
 Qy 1289 TATCAATGGTGGCTTATC---AAGGAAGAGTCCCTTATCCAGGCGCAGGACTTGTCCC 1345
 Db 1487 TCTGTTTGGACAGAGTTCCGAGAGACAAAGTCCAAAGCAAGCTGGCTGTGTCGA 1546
 Qy 1346 AGCAAAACATTT---GGTGTGTTGACTCTCAAAAGACCTTCTGATGATGTTATAAC 1402
 Db 1547 AAACACGCGCTTCCGGAAGCTTATAAACTCCATCGATTTCCGGATGAAACTCTGTCA 1606
 Qy 1403 TTTGCAAGAGTATCCAGCCATGTAATCCAGTGTTCCTATGAACATCCGCCCAATA 1462
 Db 1607 TTCAATCAATCTCATCCCTGATGGACTCTGCCGTTCCACCCATGCCGATGAGCCCTGG 1666
 Qy 1463 GTGATCAAAACGGATGTAAATATCAATTTTACAAATTTGCTAGACCGAGTGGATGCA 1522
 Db 1667 TTCAAAAGACTCGGGTCAGGTACAGACTCAGCGCATCTCAGTGACCATTCAGCCGGA 1726
 Qy 1523 GAAGTGGACAGTATGATGTTTATGTTTATCGGAACAGATGTTGGACCGTCTTAAAGTA 1582
 Db 1727 CCTTACCAGAACTACACAGTCTATTTGTTGGCTCTGAAAGTGGATGTTAAAGTT 1786
 Qy 1583 GTTTCAA 1589
 Db 1787 CTGGCAA 1793

RESULT 14
 US-09-300-958A-24
 ; Sequence 24, Application US/09300958A
 ; Patent No. 6495319
 ; GENERAL INFORMATION:
 ; APPLICANT: McClelland, Michael
 ; APPLICANT: Welsh, John
 ; APPLICANT: Trenkle, Thomas
 ; TITLE OF INVENTION: Reduced Complexity Nucleic Acid Targets and Methods of
 ; FILE OF INVENTION: Using Same
 ; FILE REFERENCE: P-PH 3457
 ; CURRENT APPLICATION NUMBER: US/09/300,958A

Query Match 3.1%; Score 84; DB 4; Length 2433;
 Best Local Similarity 47.6%; Pred. No. 1.6e-15;
 Matches 357; Conservative 0; Mismatches 375; Indels 18; Gaps 3;
 Qy 356 AACAGCTCCAGTTATCATCTTCTTCTTGGATGAGAACGGAGTAGGCTGTATGTGA 415
 Db 34 AACATCTCCAACTACACGGCCCTTCTCTGAGCCAGGATGAAAGACGCTGTATGTGGG 93
 Qy 416 GCAAAGGATCATATTTTCA-----TTGACCTGTGTTAATATCAAGGATTTT 463
 Db 94 GCCCGAGAGCCCTTCTTGGACTTAACAGCAACCTCAGCTTCTGCCAGGGGGAGTAC 153
 Qy 464 CAAAGATGTGTGCCAGTATCTTACACAGAAAGATGAATGCAAGTGGGCTGGAAAA 523
 Db 154 CAAGAGCTACTGTGAGTGCAGATGCTCAACAGGAAGCAGCAGTGCAGCTTCAAGGGCAAG 213
 Qy 524 GACATCTGAAAGATGTGCTAATTTTCATCAAGTACTTAAAGCATATAATCAGACTCAC 583
 Db 214 GACCAAGCGTGTACTGTCAAACTCATCAAGATCTCTCTGCCACTCAGCAGCAGCCAC 273
 Qy 584 TTGACGCTCTGGAACGGGGCTTTTCATCCAAATTTGCACCTACATTTGAAATTTGGACAT 643
 Db 274 CTGCTCACCTGTGACACGGCGCTTCCAGCCCTGTGTGCTTACATTCACATAGCGAGC 333
 Qy 644 CATCTGAGGACATATTTTAACTGAGGAGACTCACAATTTGAAACGGCGCGTGGGAAG 703
 Db 334 TTTACTTTAGCCCA---AGATGAGCGCGGTAATGCTATCTGAGGATGCAAGGGTCTAT 390
 Qy 704 AGTCCATATGACCCCTAAAGCTCTCAGCAGCATCCCTTTTAAATAGATGAGAAATATATCTCT 763
 Db 391 TGTCCCTTTGACCCCACTTCAAGTCCACGGCTCTGTGTGTTGATGTTGAGCTGTACACT 450
 Qy 764 GGAATCTGAGCTGATTTTATGGGCGGAGACTTTGCTATCTTCCGAATCTTTGGCACCAC 823
 Db 451 GGAACAGTCACTAGTCTTCCAGGAAACGACCCAGCCATTTCCCGGAGCCAGAGTTCCCGC 510
 Qy 824 CACCAATATCAGGACAGAGCAGCATGATTCAGGTGGTCAATG---ATCCAAAGTTTCAAT 880
 Db 511 CCCACCAAGACTGAGAGCTCCCTCACTGGCTACAGACCCCTCCCTTTGTGGCTCGGCT 570
 Qy 881 AGTCCCACTCATCTCAGAGAGTGAACAATCTCTGAGATGACAAAGTATATCTTTTCTTC 940
 Db 571 ACGTCCCGGAGAGCTGGGCGAGCCCATAGTGTATGATGATAGATCTACTTCTTCTTCTTC 630
 Qy 941 CGTGAATATGCAATAGATGAGAGACTCTGGAAGACTACTCAGCTAGAAAGTGGTCAAG 1000
 Db 631 AGCGAGCGGCGCAGGAGTTGATTTCTTTGAGAACACCATCTGCTGCCAGTTGCCGA 690
 Qy 1001 ATATGCAAGATGATTTTGGAGGCGCAGAAAGTCTGTGTAATAATGGAACAACTTCTTC 1060
 Db 691 GTCTGTAAAGGCGGATGAGGTTGAGAGCGGGTGTTCAGCAAGCGCTGGACCTCTTCTTC 750
 Qy 1061 AAAGCTCGTCTGATTTGCTCAGTCCAGGT 1090
 Db 751 AAGGCTAGCTCTGTGCTCCCGGCGCTGAT 780

US-08-556-422A-1

; Sequence 1, Application US/08556422A

; Patent No. 6576754

; GENERAL INFORMATION:

; APPLICANT: HALL, Kathryn T.

; APPLICANT: FREEMAN, Gordon J.

; APPLICANT: SCHULTZE, Joachim L.

; APPLICANT: BOUSSIOS, Vassiliki

; APPLICANT: NADLER, Lee M.

; TITLE OF INVENTION: NUCLEIC ACIDS ENCODING CD100 MOLECULES

; FILE REFERENCE: DFN-005CEA2

; CURRENT APPLICATION NUMBER: US/08/556.422A

; CURRENT FILING DATE: 1995-11-09

; NUMBER OF SEQ ID NOS: 7

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 1

; LENGTH: 4157

; TYPE: DNA

; ORGANISM: Homo sapiens

; FEATURE:

; NAME/KEY: CDS

; LOCATION: (88)...(2673)

US-08-556-422A-1

Query Match 3.1%; Score 83.2; DB 4; Length 4157;

Best Local Similarity 49.0%; Pred. No. 4.2e-15;

Matches 619; Conservative 0; Mismatches 569; Indels 75; Gaps 12;

QY	352	GGCCAAACAGCTCCAGTTATCATACCTCTCTTTGGATGAGGAACGGAGTAGCGTGTATGT	411
DB	219	GCCAGACATCTACACTACTCAGCTTCTGCTGAGCGAGGACGACACCTTGTACAT	278
QY	412	TGGAGCAAGATGCTAATTTTCAATTCGACTCTGGTTAATAT---CAAGATTTTCAAAA	468
DB	279	AGGTCCCGGAGGGGGCTTCGCTGTGAACGCACTCAACATCTCCGAGAGCAGCATGA	338
QY	469	GATTGTGGCCAGTATCTTACACAGAGAGATCAATGCAAGTGGCTGGAAGACAT	528
DB	339	GGTGTATTGGAAGGTCTCAGAGACAAAAGCAAAATGTGCAAAAAGGGGAAATCAAA	398
QY	529	CCTGAAGAAGATGTGCTAATTTTCAATCAAGTACTTAAAGGCATATATCAGACTCTTGTGA	588
DB	399	ACAGACAGAGTGCCTCAACTACATCCGGGTGCTGAGCCACTCAGCGCCACTTCCCTTTA	458
QY	589	CGCTGTGGAACGGGGCTTTTCATCCAAATTTGCACCTACATTTGAATTTGACATATCC	648
DB	459	CGTGTGGGACCAACGCAATTCACGCGGCTGTGACCACTGAATTAATC-----	512
QY	649	TGAGGACAAATATTTTAAAGCTGGAGAACTCACAATTTTGAACCGCGCTGGGAAGATCC	708
DB	513	-----CTTTAAGTTTCTGGGAAAA-----TGAAGATGGCAAGGAAGATGTC	557
QY	709	ATATGACCTAAGCTGTGACAGCATCCCTTTTAAATAGATGGAGAAATATCTCTGGAAC	768
DB	558	CTTTGACCCAGCACACAGCTACATCCGTCATGCTGATGTTGATGAGAACTTTATTCGGGAC	617
QY	769	TGCACGTATTTTATGGGGGAGACTTTGCTATCTTCGAACTCTTGGGCACCAACCC	828
DB	618	GTGCTATATTTTGGGAAGTGAACCCATCATCTCCCGAAATCT---TCCACAGTCC	674
QY	829	AATCAGGACAGACAGCATGATTCAGGTGGCTCAATGATCCAAAGTTTCAATAGTGCCCA	888
DB	675	TCAGGAGACAG---AATATGCAATCCCTTGGCTGAACGAGCTAGTTTCGTTTGTCTGA	731
QY	889	CCTCAT-----CTCAGAGAGTGAACAATCTCTGAAGATGACAAAGTATATCTTTCTT	939
DB	732	CGTGATCCGAAACCCAGACAGCCCGGAGGAGATGACAGGGGTCTACTTCTCTT	791
QY	940	CCGTGAAATGCAATAGATGGAACACTCTGGAAGAACTACTCAGCTAGATAGGTCA	999
DB	792	CACGAGGTGTCTGTGGAGTATGAGTTTGTGTTCAGGGTGTGATCCACCGATAGCAAG	851
QY	1000	GATATGCAAGATGACTTTGGAGGCGCACAGAAAGTCTGGTGAATTAATGGAACAATTCCT	1059

Search completed: September 23, 2004, 01:36:28
Job time : 205 secs

DB	852	AGTGTCAAAGGGGAGCCAGGCGGCTGAGGACCTTCAGAGAAGAAATGACCTCTCTCT	911
QY	1060	CAAGCTCTCTGATTTGCTCAGTGCAGGTCCAAATGGCATTGACACTCATTTGATGA	1119
DB	912	GAAAGCCCGACTCATCTGCTCCCGGCAG-----CAGGGTTTGGTCTTCAATGT	962
QY	1120	ACTGCAGAGTGTATTCCTAATGAACCTTTAAAGATCCTAAAAATCCAGTTGTATGGAGT	1179
DB	963	GCTGCGGATGCTTCTGCTCAGGTCCCGGCTGAAGGTGCTGTCTTATGCACT	1022
QY	1180	GTTTACGACTTCCAGTAAATTTTCAAGGATCAGCCGTGTGTATGATAGTATGATGA	1239
DB	1023	CTTCAACCCACAGCTGAACACAGTGGGGCTGTGCGCAGTGTGCGCTACAACCTGTCCAC	1082
QY	1240	TGTGAGAAGGTGTTCC-----TTGGTCCATATGCCACAG-GGATGGAGCCCAA	1287
DB	1083	AGCCGAGGAGGTCTTCTCCACGGGAAGTACATGCAGAGCACACAGTGGAGCAGTCCCA	1142
QY	1288	CTATCAATGGGTGCTTATCAAGGAAGAGTCCCTTATCCAGGCGCAGGAACTTGTCCCAG	1347
DB	1143	CACCAAGTGGTGGCTATAATGGCCCGGTACCCAGCGCGCTTGGAGCGTGCATCGA	1202
QY	1348	CAAAACATTTGGTGGTGTGACTCTACAAA-----GGACCTTCTCTGATGATGTTATAAC	1401
DB	1203	CAGCGAGGACGGGCGCCCAACTACACAGCTCTTGAATTTGCCAGACAAGACGCTGCA	1262
QY	1402	CTTTGCAAGAAGTCAATCCAGTGTTCCTATGAAACAATCGCCCAAT	1461
DB	1263	GTTTCGTTAAAGACCACTTGTGATGATGACTCGGTAAACCCCAATAGACAAGGCCAG	1322
QY	1462	AGTGATCAAAACGGATGTAATTAATTAACAATAATTCGATAGACCGAGTGGATGC	1521
DB	1323	GTTTAAATCAAGAAAGATGTGAACCTAC-----ACCCAGATCGTGGTGGACCGGACCCAGGC	1376
QY	1522	AGAAGATGGACAG---TATGATGTTATGTTTATCGGAACAGATGTTGGACCGTCTTAA	1578
DB	1377	CCTGATGGAGTGTCTATGATGTCATGTTTGTACACACAGCCCGGGAGCTTCGACAA	1436
QY	1579	AG 1580	
DB	1437	AG 1438	

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